

GenCore version 5.1.6
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CM nucleic - nucleic search, using sw model

Run on: June 19, 2004, 01:57:22 ; Search time 1844 Seconds
(without alignments)
7027.131 Million cell updates/sec

Title: US-09-019-441A-1_COPY_58_390

Perfect score: 333
Sequence: 1 cagctgccccgactcagcc.....cccggttgacgctcctaggt 333

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 2933116

Minimum DB seq length: 0
Maximum DB seq length: 333

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl :

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.ov.*
- 5: gb.pat.*
- 6: gb.ph.*
- 7: gb.pl.*
- 8: gb.pr.*
- 9: gb.ro.*
- 10: gb.scs.*
- 11: gb.sy.*
- 12: gb.un.*
- 13: gb.vi.*
- 14: gb.ba.*
- 15: em.fun.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.om.*
- 21: em.or.*
- 22: em.ov.*
- 23: em.pat.*
- 24: em.ph.*
- 25: em.pl.*
- 26: em.ro.*
- 27: em.sts.*
- 28: em.un.*
- 29: em.vi.*
- 30: em.htg.hum.*
- 31: em.htg.in.*
- 32: em.htg.other.*
- 33: em.htg.mus.*
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- 35: em.htg.rod.*
- 36: em.htg.mam.*
- 37: em.htg.vrt.*
- 38: em.sy.*
- 39: em.htgo.hum.*
- 40: em.htgo.mus.*
- 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	289.8	87.0	333	9	AB064024	AB064024 Homo sapi
2	289.8	87.0	333	9	HSJ399863	AJ399863 Homo sapi
3	288.2	86.5	333	9	AB064000	AB064000 Homo sapi
4	287.8	86.4	331	9	HSJ006162	AJ006162 Homo sapi
5	286.8	86.1	330	9	AF194592	AF194592 Homo sapi
6	286.8	86.1	330	9	AF194604	AF194604 Homo sapi
7	286.6	86.1	333	9	AB063978	AB063978 Homo sapi
8	286.6	86.1	333	9	HSJGLCVR	X95739 H.sapiens m
9	285.2	85.6	330	9	AF194579	AF194579 Homo sapi
10	285.2	85.6	330	9	AF194586	AF194586 Homo sapi
11	285.2	85.6	330	9	AF194587	AF194587 Homo sapi
12	285.2	85.6	330	9	AF194589	AF194589 Homo sapi
13	285.2	85.6	330	9	AF194605	AF194605 Homo sapi
14	285.2	85.6	330	9	AF194608	AF194608 Homo sapi
15	285.2	85.6	333	9	HSJ06676	U76676 Homo sapien
16	284.6	85.5	331	9	HSJ249377	AJ249377 Homo sapi
17	283.6	85.2	330	9	AF194595	AF194595 Homo sapi
18	283.6	85.2	330	9	AF194603	AF194603 Homo sapi
19	283.6	85.2	330	9	AF194607	AF194607 Homo sapi
20	283.4	85.1	333	9	HSJ84836	Z84836 H.sapiens g
21	282	84.7	330	9	AF194557	AF194557 Homo sapi
22	282	84.7	330	9	AF194596	AF194596 Homo sapi
23	282	84.7	330	9	AF194609	AF194609 Homo sapi
24	282	84.7	330	9	HSJ243109	AJ243109 Homo sapi
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26	281.8	84.6	333	9	AB064017	AB064017 Homo sapi
27	281.4	84.5	333	9	HSJ496502	AJ496502 Homo sapi
28	280.8	84.3	333	6	AXL67727	AXL67727 Sequence
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30	280.4	84.2	330	9	AF194541	AF194541 Homo sapi
31	280.4	84.2	330	9	AF194543	AF194543 Homo sapi
32	280.4	84.2	330	9	AF194547	AF194547 Homo sapi
33	280.4	84.2	330	9	AF194548	AF194548 Homo sapi
34	280.4	84.2	330	9	AF194552	AF194552 Homo sapi
35	280.4	84.2	330	9	AF194553	AF194553 Homo sapi
36	280.4	84.2	330	9	AF194566	AF194566 Homo sapi
37	280.4	84.2	330	9	AF194571	AF194571 Homo sapi
38	280.4	84.2	330	9	AF194573	AF194573 Homo sapi
39	280.4	84.2	330	9	AF194580	AF194580 Homo sapi
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ALIGNMENTS

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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

AB064024
Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLJ
region, partial cds, clone:LI53.
AB064024
AB064024.1 GI:21669254
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Akahori, Y., Iba, Y., Morino, K., Shinohara, M., Hirono, Y., Kakita, M.,
Suzuki, K., Torii, H., Ukai, Y., Honda, T., Katsumi, H., Okada, J.,

333 bp mRNA linear PRI 02-JUL-2002
Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLJ
region, partial cds, clone:LI53.

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Db	1	CAGTCGCCCTGACTCAGCCCTCGCTCAGTCTCCGGGTCTCTGGACAGTCAGTCACCAATC	60	
QY	61	TCCTGCACCTGGAACACGACGATGAGTTGGTGTATTAACATATGTCTCTGGTACCAAC	120	
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Query Match	86.1%;	Score 286.6; DB 9; Length 333;

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Matches 304; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

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QY 61 TCTGCACTGGACCAAGGAGTGGTGGTGTATTAACATATGTCTCTGGTACCAACAC 120
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Db 181 TCTGATCGCTTCTGTGCTCAAGTCTGCAACAGCGCTCCCTGACCATCTCTGGGCTC 240
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QY 241 CAGGCTGAGGAGGAGGCTGATTATTAATGCTGCTATATAGAGCAGCAGTCTGGGTG 300
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Db 241 CAGGCTGAGGAGGAGGCTGATTATTAATGCTGCTATATAGAGCAGCAGTCTGGGTG 300
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QY 301 TTCGGAAGAGGAGGAGGCTGACCGTCTAGGT 333
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DEFINITION Homo sapiens clone 1034 immunoglobulin lambda light chain variable
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ACCESSION AF194579
VERSION AF194579.1 GI:6643156
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 330)
AUTHORS Ignatovich, O., Tomlinson, I.M., Popov, A.V., Bruggemann, M. and
Winter, G.
TITLE Dominance of intrinsic genetic factors in shaping the human
JOURNAL immunoglobulin V-lambda repertoire
MEDLINE J. Mol. Biol. 294 (2), 457-465 (1999)
PUBMED 10610771
REFERENCE 2 (bases 1 to 330)
AUTHORS Ignatovich, O., Tomlinson, I.M., Popov, A.V., Bruggemann, M. and
Winter, G.
TITLE Direct Submission
JOURNAL Submitted (13-OCT-1999) Laboratory of Molecular Biology, MRC, Hills
Road, Cambridge CB2 2QH, UK
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Best Local Similarity 91.5%; Pred. No. 1.3e-72;
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QY 181 TCTGATCGCTTCTCTGGCTCCAAAGTCTGCAACAGCGGCTCCCTGACCATCTCTGGGCTC 240
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DB 301 TTCGAGAGGAGGACCGGCTGACCGTCTTA 330

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ACCESSION AF194587
VERSION AF194587.1 GI:6643172
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 330)
Ignatovich,O., Tomlinson,I.M., Popov,A.V., Bruggemann,M. and Winter,G.
Dominance of intrinsic genetic factors in shaping the human immunoglobulin lambda repertoire
J. Mol. Biol. 294 (2), 457-465 (1999)
20079509
10610771
PUBMED
REFERENCE 2 (bases 1 to 330)
Ignatovich,O., Tomlinson,I.M., Popov,A.V., Bruggemann,M. and Winter,G.
Direct Submission
Submitted (13-OCT-1999) Laboratory of Molecular Biology, MRC, Hills Road, Cambridge CB2 2QH, UK
FEATURES
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Query Match 85.6%; Score 285.2; DB 9; Length 330;
Best Local Similarity 91.5%; Pred. No. 1.3e-72;
Matches 302; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1 CAGTCTGCCCGGACTCAGCCTCCCTCTGCTGGTCTCTGGACAGTCTGACCATC 60
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RESULT 12
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ACCESSION AF194589
VERSION AF194589.1 GI:6643176
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 330)
Ignatovich,O., Tomlinson,I.M., Popov,A.V., Bruggemann,M. and Winter,G.
Dominance of intrinsic genetic factors in shaping the human immunoglobulin lambda repertoire
J. Mol. Biol. 294 (2), 457-465 (1999)
20079509
10610771
PUBMED
REFERENCE 2 (bases 1 to 330)
Ignatovich,O., Tomlinson,I.M., Popov,A.V., Bruggemann,M. and Winter,G.
Direct Submission
Submitted (13-OCT-1999) Laboratory of Molecular Biology, MRC, Hills Road, Cambridge CB2 2QH, UK
FEATURES
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	Best Local Similarity	91.5%	Pred. No. 1.3e-72;		
	Matches 302;	Conservative 0;	Mismatches 28;	Indels 0;	Gaps 0;
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DB	61	TCCTGCACTGGAACACGAGTGGTGGTGTATTAATATGCTCTCTGGTACCAACAC	120		
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VERSION					
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SOURCE					
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
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1 (bases 1 to 330)					
AUTHORS					
Ignatovich,O., Tomlinson,I.M., Popov,A.V., Bruggemann,M. and					
Winter,G.					
TITLE					
Dominance of intrinsic genetic factors in shaping the human					
immunoglobulin Vlambda repertoire					
J. Mol. Biol. 294 (2), 457-465 (1999)					
JOURNAL					
MEDLINE					
PUBMED					
10610771					
REFERENCE					
2 (bases 1 to 330)					
AUTHORS					
Ignatovich,O., Tomlinson,I.M., Popov,A.V., Bruggemann,M. and					
Winter,G.					
TITLE					
Direct Submission					
Submitted (13-OCT-1999) Laboratory of Molecular Biology, MRC, Hills					
Road, Cambridge CB2 2QH, UK					
JOURNAL					
FEATURES					
Location/Qualifiers					
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Query Match      85.6%; Score 285.2; DB 9; Length 330;
Best Local Similarity 91.5%; Pred. No. 1.3e-72;
Matches 302; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
QY 1 CAGTCTGCCCGGACATCAGCCCTCCCTCTGTCTGTGGTCTCTCGACAGTCGGTCAACATC 60
DB 1 CAGTCTGCCCGGACATCAGCCCTCCCTCTGTCTGTGGTCTCTCGACAGTCGGTCAACATC 60
QY 61 TCCTGCACTGGAAACAGAGGATGACGTTGGTGGTTAACTATGTCTCTGGTACCAACAC 120
DB 61 TCCTGCACTGGAAACAGAGGATGACGTTGGTGGTTAACTATGTCTCTGGTACCAACAC 120
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RESULT 15
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ACCESSION U76676
VERSION U76676.1 GI:1673590
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 333)
AUTHORS Aguilera, I., Melero, J., Nunez-Roldan, A. and Sanchez, B.
TITLE Molecular structure of eight human autoreactive monoclonal
antibodies
JOURNAL Immunology 102 (3), 273-280 (2001)
MEDLINE 21195372
PUBMED 11298825
REFERENCE 2 (bases 1 to 333)
AUTHORS Aguilera, I.
TITLE Direct Submission
JOURNAL Submitted (30-OCT-1996) Hospital U. Virgen del Rocío, Immunology,
Manuel Siurot s/n, Seville, Spain, 41013
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CDS
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ORIGIN
Query Match      85.8%; Score 285; DB 9; Length 333;
Best Local Similarity 91.0%; Pred. No. 1.5e-72;
Matches 303; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
QY 1 CAGTCTGCCCGGACATCAGCCCTCCCTCTGTCTGTGGTCTCTCGACAGTCGGTCAACATC 60
DB 1 CAGTCTGCCCGGACATCAGCCCTCCCTCTGTCTGTGGTCTCTCGACAGTCGGTCAACATC 60
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Search completed: June 19, 2004, 04:01:33
Job time : 1847 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using **sw** model

Run on: June 19, 2004, 01:55:31 ; Search time 276 Seconds
(without alignments)
5125.543 Million cell updates/sec

Title: US-09-019-441a-1_COPY_58_390

Perfect score: 333

Sequence: 1 cagctgcccgcactgagcc.....cccggtgacgcgtcctaggt 333

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 4156560

Minimum DB seq length: 0

Maximum DB seq length: 333

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq 29Jan04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2003as:*
- 8: Geneseqn2003bs:*
- 9: Geneseqn2003cs:*
- 10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	280.8	84.3	333	4	Ah42407 Nucleotid
2	280.8	84.3	333	4	Ah42407 Nucleotid
3	275.8	82.8	330	6	Abx00191 Mouse DNA
4	275.8	82.8	330	6	Abk71397 Thrombopo
5	275.4	82.7	333	2	Aat10327 Human ant
6	275.4	82.7	333	2	Aaz31655 Coding se
7	273.8	82.2	333	2	Aaz31654 Coding se
8	270.8	81.3	330	4	Aas03477 DNA encod
9	269.2	80.8	330	4	Aas03520 DNA encod
10	265.8	79.8	333	2	Aaq55659 Monoclonal
11	262.8	78.9	330	8	Acc85452 Human gly
12	248.4	74.6	327	4	Aaf58706 Huntingtin
13	243.6	73.2	330	6	Aad46293 Human KDR
14	243.6	73.2	330	7	Aad23328 VEGF bind
15	243.6	73.2	330	9	Ad24421 Human lig
16	243.6	73.2	330	9	Ad80798 Human clo
17	242.7	72.7	330	6	Aad46298 Human KDR
18	242.7	72.7	330	7	Abt23333 VEGF bind
19	242.7	72.7	330	9	Ad24431 Human lig
20	242.7	72.7	330	9	Ad80808 Human KDR
21	239.6	72.0	324	5	Ab68682 Human ant
22	239.6	72.0	324	8	Ac45346 Anti-Rh(D
23	239.2	71.8	300	3	Aaa52443 Wild-type

24	237	71.2	294	4	ABA70898	Human foe
25	237	71.2	294	4	AAI51083	Probe #19
26	237	71.2	294	4	ABA37341	Probe #15
27	237	71.2	294	4	AAK45127	Human bon
28	237	71.2	294	4	AAK19166	Human bra
29	237	71.2	294	4	ABS44798	Human liv
30	237	71.2	294	6	ABS19377	Human gen
31	234.4	70.4	300	3	AA52446	High affi
32	230	69.1	279	3	AA56720	HuIgIambd
33	228	68.5	300	3	AA56720	Streptativ
34	227.4	68.3	333	4	AA503506	DNA encod
35	220.8	66.3	283	3	AA56719	Human Ig
36	212.4	63.8	279	3	AA56724	HuIgIambd
37	211.2	63.4	283	3	AA56723	Human Ig
38	208.8	62.7	312	5	AAH68683	Human ant
39	208.8	62.7	312	8	ACD45347	Anti-Rh(D
40	202	60.7	330	8	ADA99167	Human ant
41	201.8	60.6	330	4	AA503527	DNA encod
42	201.4	60.5	331	4	AAI68771	Human ant
43	198.6	59.6	330	4	AA503458	DNA encod
44	198.4	59.6	333	4	AA503485	DNA encod
45	197	59.2	330	4	AA503529	DNA encod

ALIGNMENTS

RESULT 1

AAH42407
ID AAH42407 standard; DNA; 333 BP.

XX AC AAH42407;

XX DT 01-OCT-2001 (first entry)

XX DB Nucleotide sequence of variable light chain fragment of clone G102.

XX KW Antibody; light chain; VL; amyloid protein; blood brain barrier;
endothelial cell; brain cell antigen; inflammation; adhesion molecule;
transferrin receptor; neurological disease; Alzheimer's disease;
prion disease; AIDS-related dementia; epilepsy; brain injury; ss.

XX OS Homo sapiens.

XX FN WO200144300-A2.

XX PD 21-JUN-2001.

XX PF 27-NOV-2000; 2000WO-GB004501.

XX PR 13-DEC-1999; 99US-0170599P.

XX PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX PI Webster C, Osbourn J, Ward G, Miller K;

XX DR WPI: 2001-398131/42.

XX P-PSDB; AAG62963.

XX PT Mixture or panel of antibodies for selecting specific binding members
that cross the blood brain barrier, for use in delivering different
molecules and treating neurological diseases.

XX PS Disclosure; Page 106; 109pp; English.

XX CC The present sequence encodes an antibody variable light chain (VL)
fragment. The fragment is used to produce a mixture or panel of 5
different specific binding members, each comprising an antibody VH and/or
VL variable domain and capable, when displayed on the surface of
filamentous bacteriophage particles or in the case of a specific binding
member comprising the D5 VH and/or VL variable domain when bound to human
serum amyloid protein, to pass through a mammalian blood brain barrier
(BBB). The panel is useful for the selection of specific binding members

CC with a desired property such as ability to cross BBB, ability to bind
CC endothelial cells or other brain cell antigen, ability to bind areas of
CC inflammation in the brain or BBB breakdown or ability to bind
CC intracellular adhesion molecules and to bind transferrin receptor. The
CC antibodies are useful in diagnosis, prophylaxis and treatment of human or
CC animal body, including neurological diseases, such as Alzheimer's
CC disease, prion disease, AIDS-related dementia, epilepsy and traumatic
CC brain injury and any diseases involving inflammation occurring within the
CC brain or central nervous system
XX
SQ Sequence 333 BP; 72 A; 99 C; 86 G; 76 T; 0 U; 0 Other;

Query Match 84.3%; Score 280.8; DB 4; Length 333;
Best Local Similarity 90.4%; Pred. No. 4.8e-78;
Matches 300; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
Qy 1 CAGCTGCGCCGAGCTCAGCTCCCTCTGCTGGTCTCTCTGACAGTGGTCAACATC 60
Db 1 CAGCTGCTGCTGACTCAGCTCCCTCTGCTGGTCTCTCTGACAGTGGTCAACATC 60
Qy 61 TCCTGCACTGGAACAGGAGTACGTTGGTGGTTATTAATGTTCTCTGGTACCAACAC 120
Db 61 TCCTGCACTGGAACAGGAGTACGTTGGTGGTTATTAATGTTCTCTGGTACCAACAA 120
Qy 121 CACCCAGGCAAGCCGCCAACTCATGTTATGATGTGGTAAAGCGGCTCAGGGGTC 180
Db 121 CACCCAGGCAAGCCGCCAACTCATGTTATGAGGGCAGTAGCGGCTCAGGGGTT 180
Qy 181 TCTGATGCTTCTCTGGCTCCAACTGCGCAACAGCGCTCCCTCTGACATCTCTGGGCTC 240
Db 181 TCTAATGCTTCTCTGGCTCCAACTGCGCAACAGCGCTCCCTCTGACATCTCTGGGCTC 240
Qy 241 CAGCTGAGGACGAGGCTGATTATGTTGTTTCATATACACACAGTACGATCTTGTTA 300
Db 241 CAGCTGAGGACGAGGCTGATTATGTTGTTTCATATACACACAGTACGATCTTGTTA 300
Qy 301 TTCGGAAGAGGACCGGTTGACCGTCTCTAGG 332
Db 301 TTCGCGGAGGACCAAGCTGACCGTCTCTAGG 332

RESULT 2
AAH42401
ID AAH42401 standard; DNA; 333 BP.
XX
AC AAH42401;
XX
DT 01-OCT-2001 (first entry)
XX
DE Nucleotide sequence of variable light chain fragment of clone G93.
XX
KW Antibody; light chain; VL; amyloid protein; blood brain barrier;
KW endothelial cell; brain cell antigen; inflammation; adhesion molecule;
KW transferrin receptor; neurological disease; Alzheimer's disease;
KW prion disease; AIDS-related dementia; epilepsy; brain injury; ss.
XX
OS Homo sapiens.
XX
PN WO200144300-A2.
XX
PD 21-JUN-2001.
XX
PF 27-NOV-2000; 2000WO-GB004501.
XX
PR 13-DEC-1999; 99US-0170599P.
XX
PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Webster C, Osbourn J, Ward G, Miller K;
XX
DR WPI; 2001-398131/42.
XX
P-PSDB; AAG62957.

PT Mixture or panel of antibodies for selecting specific binding members
PT that cross the blood brain barrier, for use in delivering different
PT molecules and treating neurological diseases.
XX
XX Disclosure; Page 103; 109pp; English.
XX
XX The present sequence encodes an antibody variable light chain (VL)
CC fragment. The fragment is used to produce a mixture or panel of 5
CC different specific binding members, each comprising an antibody VH and/or
CC VL variable domain and capable, when displayed on the surface of
CC filamentous bacteriophage particles or in the case of a specific binding
CC member comprising the DS VH and/or VL variable domain when bound to human
CC serum amyloid protein, to pass through a mammalian blood brain barrier
CC (BBB). The panel is useful for the selection of specific binding members
CC with a desired property such as ability to cross BBB, ability to bind
CC endothelial cells or other brain cell antigen, ability to bind areas of
CC inflammation in the brain or BBB breakdown or ability to bind
CC intracellular adhesion molecules and to bind transferrin receptor. The
CC antibodies are useful in diagnosis, prophylaxis and treatment of human or
CC animal body, including neurological diseases, such as Alzheimer's
CC disease, prion disease, AIDS-related dementia, epilepsy and traumatic
CC brain injury and any diseases involving inflammation occurring within the
CC brain or central nervous system
XX
SQ Sequence 333 BP; 71 A; 99 C; 87 G; 76 T; 0 U; 0 Other;

Query Match 84.3%; Score 280.8; DB 4; Length 333;
Best Local Similarity 90.4%; Pred. No. 4.8e-78;
Matches 300; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
Qy 1 CAGCTGCGCCGAGCTCAGCTCCCTCTGCTGGTCTCTCTGACAGTGGTCAACATC 60
Db 1 CAGCTGCTGCTGACTCAGCTCCCTCTGCTGGTCTCTCTGACAGTGGTCAACATC 60
Qy 61 TCCTGCACTGGAACAGGAGTACGTTGGTGGTTATTAATGTTCTCTGGTACCAACAC 120
Db 61 TCCTGCACTGGAACAGGAGTACGTTGGTGGTTATTAATGTTCTCTGGTACCAACAA 120
Qy 121 CACCCAGGCAAGCCGCCAACTCATGTTATGATGTGGTAAAGCGGCTCAGGGGTC 180
Db 121 CACCCAGGCAAGCCGCCAACTCATGTTATGAGGGCAGTAGCGGCTCAGGGGTT 180
Qy 181 TCTGATGCTTCTCTGGCTCCAACTGCGCAACAGCGCTCCCTCTGACATCTCTGGGCTC 240
Db 181 TCTAATGCTTCTCTGGCTCCAACTGCGCAACAGCGCTCCCTCTGACATCTCTGGGCTC 240
Qy 241 CAGGCTGAGGACGAGGCTGATTATGTTGTTTCATATACACACAGTACGATCTTGTTA 300
Db 241 CAGGCTGAGGACGAGGCTGATTATGTTGTTTCATATACACACAGTACGATCTTGTTA 300
Qy 301 TTCGGAAGAGGACCGGTTGACCGTCTCTAGG 332
Db 301 TTCGCGGAGGACCAAGCTGACCGTCTCTAGG 332

RESULT 3
ABX00191
ID ABX00191 standard; DNA; 330 BP.
XX
AC ABX00191;
XX
DT 20-DEC-2002 (first entry)
XX
DE Mouse DNA encoding MPL 12E10L.
XX
KW ds; gene; monoclonal antibody; signal transduction agonist; cancer;
KW inflammatory disease; dysendocrinism; blood disease; leukaemia;
KW cytostatic; antiinflammatory; immunosuppressive; immunostimulant;
KW hormonal disorder; diabetes; diabetes; autoimmune disease.
XX
OS Mus sp.
XX
PN WO200233073-A1.

XX PD 25-APR-2002.
XX PF 22-OCT-2001; 2001WO-JP009260.
XX PR 20-OCT-2000; 2000JP-00321821.
XX PR 20-OCT-2000; 2000JP-00321822.
XX PR 12-MAR-2001; 2001WO-JP001912.
XX PR 17-APR-2001; 2001WO-JP003288.
XX PR 12-SEP-2001; 2001JP-00277314.
XX PA (CHUS) CHUGAI SEIYAKU KK.
XX PI Fukushima N, Tsuchiya M, Uno S, Ontomo T, Yabuta N, Tsunoda H;
XX DR WPI; 2002-682599/73.
XX DR P-PSDB; ABC97830.
XX PT Modified single chain multimeric Fv antibody acting as a signal
XX PT transduction agonist for treatment of inflammatory hormonal and blood
XX PT disorders and cancer.
XX PS Example 8; Page 202; 217pp; Japanese.
XX CC The invention relates to a new modified single chain Fv antibody
XX CC containing at least two Heavy chain variable domains and at least two
XX CC Light chain variable domains from the same or different monoclonal
XX CC antibodies and which is an agonist for crosslinking a molecule at the
XX CC cell surface or within the cell and thereby transducing a signal into the
XX CC cell. Also include are the DNA encoding the antibody, animal cells and
XX CC microorganisms transformed by and expressing the antibody, the preparation of
XX CC the antibodies by culture of the transformed cells, drug compositions
XX CC containing the antibodies and an assay method for the agonist activity of
XX CC the antibodies by contacting the antibodies with cells expressing the
XX CC relevant cell surface or internal molecule. The antibodies are useful for
XX CC treatment and prevention of cancer, inflammatory disease, hormonal
XX CC disorders including diabetes, autoimmune disease, leukaemia, a DNA
XX CC dysendocrinism and blood disorders. The present invention is a DNA
XX CC sequence encoding an antibody of the invention or a fragment thereof
XX SQ Sequence 330 BP; 73 A; 100 C; 83 G; 74 T; 0 U; 0 Other;
Query Match 82.8%; Score 275.8; DB 6; Length 330;
Best Local Similarity 90.2%; Pred. No. 1.8e-76;
Matches 295; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
Qy 4 TCTGCCCGACTCAGCCTCCCTCTGTCTGGGTCTCTCTGGACAGTGGGTCAACCATCTCC 63
Db 4 TATGTGCTGACTCGACCCACCTCGGTGTCTGAGGTCTCTCTGGACAGTGGGTCAACCATCTCC 63
Qy 64 TGCACCTGGAAACAGGATGACGTGGTGGTGTATTAACCTATGCTCTCTGGTACCAACAC 123
Db 64 TGCACCTGGAAACAGGATGACGTGGTGGTGTATTAACCTATGCTCTCTGGTACCAACAC 123
Qy 124 CCAGGCAAGGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGCTCAGGGGTCTCT 183
Db 124 CCAGGCAAGGCCCCCAAACTCATGATTTATGAGGGCAGTAAACGGCCCTCAGGGGTCTCT 183
Qy 184 GATCGCTTCTCTGGCTCCAAAGTCTGGCAACACGGCCCTCCCTGACCATCTCTGGGCTCCAG 243
Db 184 AATCGCTTCTCTGGCTCCAAAGTCTGGCAACACGGCCCTCCCTGACCATCTCTGGGCTCCAG 243
Qy 244 GCTGAGGACGAGGTGATTTACTTGTTCATATACCAACGAGTACGACTTTGTTATTC 303
Db 244 GCTGAGGACGAGGTGATTTACTTGTTCATATACCAACGAGTACGACTTTGTTATTC 303
Qy 304 GGAAGAGGAGCCCGGTGACCGTCTTA 330
Db 304 GCGGAGGAGCCAAAGCTGACCGTCTTA 330
RESULT 4
ABX71397

ID XX ABX71397 standard; DNA; 330 BP.
XX AC ABX71397;
XX DT 30-JUL-2002 (first entry)
XX DE Thrombopoietin (TPO) agonist antibody associated polynucleotide #15.
XX KW Modified antibody; thrombopoietin; TPO; agonist; TPO receptor;
XX KW platelet reduction-associated blood disease; thrombocytopenia;
XX KW cancer chemotherapy; leukaemia; signal transduction; ds.
XX OS Mus sp.
XX PN WO200233072-A1.
XX PD 25-APR-2002.
XX PF 22-OCT-2001; 2001WO-JP009259.
XX PR 20-OCT-2000; 2000JP-00321821.
XX PR 17-APR-2001; 2001WO-JP003288.
XX PR 12-SEP-2001; 2001JP-00277314.
XX PA (CHUS) CHUGAI SEIYAKU KK.
XX PI Tsuchiya M, Ontomo T, Yabuta N, Tsunoda H, Orita T;
XX DR WPI; 2002-383513/41.
XX CC Degraded thrombopoietin agonist antibodies containing H and L chain V
XX CC domains of monoclonal antibody, useful in preventives and/or remedies for
XX CC blood diseases, thrombopenia following cancer chemotherapy or leukemia.
XX PS Example 8; Page 198-199; 213pp; Japanese.
XX CC The invention describes a modified antibody comprising at least 2 heavy
XX CC chain variable domains and 2 or more light chain variable domains of an
XX CC antibody, and exhibits thrombopoietin (TPO) agonistic effect by causing
XX CC the TPO receptor to crosslink. The antibodies are useful in preventives
XX CC and/or remedies for platelet reduction-associated blood diseases,
XX CC thrombocytopenia following cancer chemotherapy or leukaemia. The antibody
XX CC can act as a TPO signal transduction agonist by transducing a signal into
XX CC cells by crosslinking a TPO receptor to exert TPO agonism. This sequence
XX CC represents thrombopoietin (TPO) agonist antibody associated
XX CC polynucleotide used in the creation of the modified antibody described in
XX CC the invention
XX SQ Sequence 330 BP; 73 A; 100 C; 83 G; 74 T; 0 U; 0 Other;
Query Match 82.8%; Score 275.8; DB 6; Length 330;
Best Local Similarity 90.2%; Pred. No. 1.8e-76;
Matches 295; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
Qy 4 TCTGCCCGACTCAGCCTCCCTCTGTCTGGGTCTCTCTGGACAGTGGGTCAACCATCTCC 63
Db 4 TATGTGCTGACTCGACCCACCTCGGTGTCTGAGGTCTCTCTGGACAGTGGGTCAACCATCTCC 63
Qy 64 TGCACCTGGAAACAGGATGACGTGGTGGTGTATTAACCTATGCTCTCTGGTACCAACAC 123
Db 64 TGCACCTGGAAACAGGATGACGTGGTGGTGTATTAACCTATGCTCTCTGGTACCAACAC 123
Qy 124 CCAGGCAAGGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGCTCAGGGGTCTCT 183
Db 124 CCAGGCAAGGCCCCCAAACTCATGATTTATGAGGGCAGTAAACGGCCCTCAGGGGTCTCT 183
Qy 184 GATCGCTTCTCTGGCTCCAAAGTCTGGCAACACGGCCCTCCCTGACCATCTCTGGGCTCCAG 243
Db 184 AATCGCTTCTCTGGCTCCAAAGTCTGGCAACACGGCCCTCCCTGACCATCTCTGGGCTCCAG 243
Qy 244 GCTGAGGACGAGGTGATTTACTTGTTCATATACCAACGAGTACGACTTTGTTATTC 303
Db 244 GCTGAGGACGAGGTGATTTACTTGTTCATATACCAACGAGTACGACTTTGTTATTC 303

QY 304 GGAAGAGGACCCGGTTGACCGTCTTA 330
 DB 304 GCGGAGGAGCAAGCTGACCGTCTTA 330

RESULT 5
 ID AAT10327 standard; cDNA to mRNA; 333 BP.
 AC AAT10327;
 XX 16-OCT-2003 (revised)
 DT 18-JUL-1996 (first entry)
 XX Human anti-Pseudomonas aeruginosa type B antibody VL region cDNA.
 DE Human; immunoglobulin; IgM; lambda light chain; variable region;
 KW lipopolysaccharide; LPS; antigen; Pseudomonas aeruginosa; type B;
 KW monoclonal antibody; ss.
 XX Homo sapiens; (cell line MP-5097).
 OS
 XX
 FH Key Location/Qualifiers
 FT CDS 1..333
 FT /tag= a
 FT /product= "VL chain"
 FT /note= "coding region does not include start or stop
 FT codons"

JP07327677-A.
 XX
 XX 19-DEC-1995.
 XX
 XX 07-JUN-1994; 94JP-00125125.
 XX 07-JUN-1994; 94JP-00125125.
 XX (MITK) MITSUI TOATSU CHEM INC.
 XX
 XX WPI; 1996-072335/08.
 XX P-PSDB; AAR89148.
 XX Gene(s) encoding human antibody variable regions against P.aeruginosa
 PT type B - useful for prodn. of monoclonal antibody-producing cells.
 XX
 PS Claim 4; Page 9; 12pp; Japanese.
 XX
 XX The present sequence encodes the light chain variable region of a human
 CC antibody which specifically recognises a lipopolysaccharide (LPS) antigen
 CC from Pseudomonas aeruginosa. The coding sequence can be used for
 CC preparing cell lines which produce monoclonal antibodies against the LPS.
 CC (Updated on 16-OCT-2003 to standardise OS field)
 XX
 SQ Sequence 333 BP; 70 A; 108 C; 77 G; 78 T; 0 U; 0 Other;
 XX
 Query Match 82.7%; Score 275.4; DB 2; Length 333;
 Best Local Similarity 89.2%; Pred. No. 2.4e-76;
 Matches 297; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 1 CAGTCTGCCGACTACGCTCCCTCTGTGCTGGTCTCTCTGACAGTGGTCAACATC 60
 DB 1 CAGTCTGCCGACTACGCTCCCTCTGTGCTGGTCTCTCTGACAGTGGTCAACATC 60
 QY 61 TCCTGCACTGGAACAGCAGTGGTGGTTATTAATGCTCTCTGTTACCAACAC 120
 DB 61 TCCTGCACTGGAACAGCAGTGGTGGTTATTAATGCTCTCTGTTACCAACAA 120
 QY 121 CACCCAGCAAGCCCAAACTCATGATTATGATGTGCTAAGCGGGCTCAGGGGTC 180
 DB 121 CACCCAGCAAGCCCAAACTCTCATTTATGATGTCTAGTATTCGGCGCTCAGGGGTT 180
 QY 181 TCTGATCGTCTCTGGTCTCAAGTCTGGCAACGCGCTCCCTGACCACTCTCGGCTC 240

DB 181 TCTGATCGTCTCTGGTCTCAAGTCTGGCAACGCGCTCCCTGACCACTCTCGGCTC 240
 QY 241 CAGGCTGAGGACGAGCTGATTATTACTGTGTTTATATACCAACGAGTCTGTGTTA 300
 DB 241 CAGGCTGAGGACGAGCTGATTATTACTGTGTTTATATACCAACGAGTCTGTGTTA 300
 QY 301 TTCGGAGAGGACCGCGTTGACCGTCTTAGGT 333
 DB 301 TTCGGAGAGGACCGCGTTGACCGTCTTAGGT 333

RESULT 6
 AAZ31655
 ID AAZ31655 standard; DNA; 333 BP.
 XX AAZ31655;
 AC AAZ31655;
 XX 13-JAN-2000 (first entry)
 DT
 XX
 DE Coding sequence for VL domain CDR of anti-estradiol antibody.
 XX
 KW Estradiol; complementarity determining region; CDR; estriol-3-sulphate;
 KW antibody antigen binding domain; steroid hormone; estriol; testosterone;
 KW dihydrotestosterone; progesterone; estriol 3-beta-di-glucuronide;
 KW menstrual cycle; hormone replacement therapy; oestrogen secreting tumour;
 KW diagnosis; VL domain; ds.
 XX
 OS Homo sapiens.
 XX
 XX US5977319-A.
 XX
 XX 02-NOV-1999.
 XX
 XX 21-OCT-1997; 97US-00958201.
 XX
 XX 21-OCT-1996; 96US-0028897P.
 XX
 XX (CAME-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 XX Johnson KS, Pope AR, Pritchard K, Williams AJ;
 XX WPI; 1999-619713/53.
 XX P-PSDB; AAV43257.
 XX
 XX New specific binding partners for estradiol, used for monitoring
 PT estradiol levels during the menstrual cycle, in hormone replacement
 PT therapy and for diagnosing estrogen secreting tumors.
 XX
 XX Disclosure; Col 27-28; 26pp; English.
 XX
 XX This sequence encodes a VL domain complementarity determining region
 CC (CDR) from an antibody specific for estradiol. The invention relates to
 CC specific binding members (sdp) comprising a polypeptide that comprises an
 CC antibody antigen binding domain (AABD) which has a dissociation constant
 CC of less than 1.0x10⁻⁸M for estradiol, and a dissociation constant of at
 CC least 500-fold higher for the steroid hormones selected from estriol,
 CC testosterone, dihydrotestosterone, progesterone, estriol-3-sulphate and
 CC estriol 3-beta-di-glucuronide, where the polypeptide comprises an
 CC antibody VH domain. The sdp can be used in an immunoassay for
 CC determining the presence or absence of estradiol in a sample. They can be
 CC used for monitoring estradiol levels, e.g. during the menstrual cycle, in
 CC hormone replacement therapy and for diagnosing oestrogen secreting
 CC tumors. The sdp can provide for discrimination between estradiol and
 CC other related steroids
 XX
 SQ Sequence 333 BP; 68 A; 101 C; 84 G; 80 T; 0 U; 0 Other;
 XX
 Query Match 82.7%; Score 275.4; DB 2; Length 333;
 Best Local Similarity 89.2%; Pred. No. 2.4e-76;
 Matches 297; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 1 CAGTCTGCCGACTACGCTCCCTCTGTGCTGGTCTCTCTGACAGTGGTCAACATC 60

Db 1 CAGTCTGCTGACTCAGCGTCTCTGTGCTGGGTCTCTGGACAGTCGATCACCATC 60
Qy 61 TCTTGCACTGGAACACAGCGATGAGCTTGGTGGTATTAACCTATGCTCTCGGTACCAAC 120
Db 61 TCTTGCACTGGAACACAGCGATGAGCTTGGTGGTATTAACCTATGCTCTCGGTACCAAC 120
Qy 121 CACCCAGGCAAGAGCCCAAACTCATGATTTATGATGCTGCTAAGCGGGCTCAGGGGTC 180
Db 121 CACCCAGGCAAGAGCCCAAACTCATGATTTATGATGCTGCTAAGCGGGCTCAGGGGTC 180
Qy 181 TCTGATCGCTTCTGCTGCTCAAGTCTGGCAACAGCGGCTCCCTGACCATCTCTGGGCTC 240
Db 181 CCTAATCGCTTCTGAGGCTCAAGTCTGGCAACAGCGGCTCCCTGACCATCTCTGGGCTC 240
Qy 241 CAGCTCAGACGAGGCTGATTTACTGTTTATATATATATATATATATATATATATATAT 300
Db 241 CAGCTCAGACGAGGCTGATTTACTGTTTATATATATATATATATATATATATATATAT 300
Qy 301 TTCGGAAGAGGAGCCCGCTTACCGTCTCTAGGT 333
Db 301 TTCGGCGAGGAGCCCAAGCTGACCGTCTCTAGGT 333

RESULT 7

AAZ31654
ID AAZ31654 standard; DNA; 333 BP.

AC AAZ31654;

DT 13-JAN-2000 (first entry)

XX Coding sequence for VL domain CDR of anti-estradiol antibody.

XX Estradiol; complementarity determining region; CDR; estradiol-3-sulphate;
XX antibody antigen binding domain; steroid hormone; estradiol; testosterone;
XX dihydrotestosterone; progesterone; estradiol 3-beta-di-glucuronide;
XX menstrual cycle; hormone replacement therapy; oestrogen secreting tumour;
XX diagnosis; VL domain; ds.

OS Homo sapiens.

XX US5977319-A.

XX 02-NOV-1999.

XX 21-OCT-1997; 97US-00958201.

XX 21-OCT-1996; 96US-0028897P.

XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Johnson KS, Pope AR, Pritchard K, Williams AJ;

XX WPI; 1999-619713/53.

XX P-PSDB; AAY43256.

XX New specific binding partners for estradiol, used for monitoring
XX estradiol levels during the menstrual cycle, in hormone replacement
XX therapy and for diagnosing estrogen secreting tumors.

XX Disclosure; Col 25-26; 26pp; English.

XX This sequence encodes a VL domain complementarity determining region
XX (CDR) from an antibody specific for estradiol. The invention relates to
XX specific binding members (abp) comprising a polypeptide that comprises an
XX antibody antigen binding domain (AABD) which has a dissociation constant
XX of less than 1.0x10⁻⁸M for estradiol, and a dissociation constant of at
XX least 500-fold higher for the steroid hormones selected from estradiol,
XX testosterone, dihydrotestosterone, progesterone, estradiol-3-sulphate and
XX estradiol 3-beta-di-glucuronide, where the polypeptide comprises an
XX antibody VH domain. The abps can be used in an immunoassay for
XX determining the presence or absence of estradiol in a sample. They can be

CC used for monitoring estradiol levels, e.g. during the menstrual cycle, in
CC hormone replacement therapy and for diagnosing oestrogen secreting
CC tumors. The abps can provide for discrimination between estradiol and
CC other related steroids

XX Sequence 333 BP; 68 A; 100 C; 84 G; 81 T; 0 U; 0 Other;

Qy Query Match 82.2%; Score 273.8; DB 2; Length 333;

XX Best Local Similarity 88.9%; Pred. No. 7.6e-76;

XX Matches 296; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

Qy 1 CAGTCTGCTGACTCAGCGTCTCTGTGCTGGGTCTCTGGACAGTCGATCACCATC 60

Db 1 CAGTCTGCTGACTCAGCGTCTCTGTGCTGGGTCTCTGGACAGTCGATCACCATC 60

Qy 61 TCTTGCACTGGAACACAGCGATGAGCTTGGTGGTATTAACCTATGCTCTCGGTACCAAC 120

Db 61 TCTTGCACTGGAACACAGCGATGAGCTTGGTGGTATTAACCTATGCTCTCGGTACCAAC 120

Qy 121 CACCCAGGCAAGAGCCCAAACTCATGATTTATGATGCTGCTAAGCGGGCTCAGGGGTC 180

Db 121 CACCCAGGCAAGAGCCCAAACTCATGATTTATGATGCTGCTAAGCGGGCTCAGGGGTC 180

Qy 181 TCTGATCGCTTCTGCTGCTCAAGTCTGGCAACAGCGGCTCCCTGACCATCTCTGGGCTC 240

Db 181 CCTAATCGCTTCTGAGGCTCAAGTCTGGCAACAGCGGCTCCCTGACCATCTCTGGGCTC 240

Qy 241 CAGCTCAGACGAGGCTGATTTACTGTTTATATATATATATATATATATATATATATAT 300

Db 241 CAGCTCAGACGAGGCTGATTTACTGTTTATATATATATATATATATATATATATATAT 300

Qy 301 TTCGGAAGAGGAGCCCGCTTACCGTCTCTAGGT 333

Db 301 TTCGGCGAGGAGCCCAAGCTGACCGTCTCTAGGT 333

RESULT 8

AA503477

ID AAS03477 standard; cDNA; 330 BP.

XX AAS03477;

XX 29-AUG-2001 (first entry)

XX DNA encoding anti-adipocyte monoclonal antibody light chain, FAT 64.

XX Antibody; adipocyte; heavy chain; light chain; obesity; FAT;
XX heart disease; complementarity determining region; CDR; ss.

XX Homo sapiens.

XX WO200127279-A1.

XX 19-APR-2001.

XX 11-OCT-2000; 2000WO-GB003900.

XX 12-OCT-1999; 99US-0158812P.

XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Edwards BM, Main SH, Vaughan TJ;

XX WPI; 2001-282031/29.

XX P-PSDB; AAU02577.

XX Panel of specific binding members of antibody molecules which bind to
XX whole adipocytes is used in the treatment of obesity and obesity related
XX diseases.

XX Disclosure; Page 140-141; 182pp; English.

XX AAS03401-AAS03535 represent anti-adipocyte monoclonal antibody heavy and


```
XX Key Location/Qualifiers
FH misc_feature 67..108
FT /*tag= a
FT /*note= "Encodes CDR 1."
FT misc_feature 154..174
FT /*tag= b
FT /*note= "Encodes CDR 2."
FT misc_feature 271..294
FT /*tag= c
FT /*note= "Encodes CDR 3."
FT misc_feature 307..342
FT /*tag= d
FT /*note= "Framework IV. J lambda 2 segment."
XX EP581353-A1.
XX 02-FEB-1994.
XX 05-JUL-1993; 93EP-00201959.
XX 03-JUL-1992; 92EP-00202032.
XX (NEW-) NEDERLANDEN MIN WELZIJN.
XX Osterhaus ADME;
XX WPI; 1994-036603/05.
XX P-PSDB; AAR45606.
XX Monoclonal antibodies to HIV-1 - directed against glycoprotein gp120,
XX useful for passive immunotherapy or prodn. of anti-idiotypic vaccines.
XX Claim 11; Page 17-18; 34pp; English.
XX The monoclonal antibodies (MAB's) designated GP13, GP44 and GP68 react
XX with HIV-1 gp120 glycoprotein variants containing the amino acids Asn88,
XX Lys117, Asn262 and Tyr 435 but exhibit at least 50% reduced reaction with
XX gp120 variants in which these amino acids have been deleted or
XX substituted. The MAB's are useful for passive immunotherapy and their
XX anti-idiotypic antibodies can be used in the production of vaccines.
XX (Updated on 25-MAR-2003 to correct FN field.) (Updated on 25-MAR-2003 to
XX correct PA field.)
XX Sequence 333 BP; 69 A; 104 C; 81 G; 79 T; 0 U; 0 Other;

Query Match 79.8%; Score 265.8; DB 2; Length 333;
Best Local Similarity 87.4%; Pred. No. 2.5e-73;
Matches 291; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 1 CAGTCTGCCCGACTCAGCCCTCCCTCTGTGCTGGTCTCTGACAGTGGTCAACCATC 60
DB 1 CAGTCTGCCCGACTCAGCCCTCCCTCTGTGCTGGTCTCTGACAGTGGTCAACCATC 60
QY 61 TCCTGCATGGAACACGAGATGACGTTGGTGGTTATTAATACTATGCTCTCTGTATCAACAC 120
DB 61 TCCTGCATGGAACACGAGATGACGTTGGTGGTTATTAATACTATGCTCTCTGTATCAACAA 120
QY 121 CACCCAGGCAAGCCCCCAACTCATGTTATGATGCTGCTAGCGGCTCAGGGGTC 180
DB 121 CACCCAGGCAAGCCCCCAACTCATGTTATGATGCTGCTAGCGGCTCAGGGGTC 180
QY 181 TCTGATGCTTCTCTGGCTCCAAAGTCTGGCAACAGCGCTCCCTGACCATCTCTGGGCTC 240
DB 181 CCTGATGCTTCTCTGGCTCCAAAGTCTGGCAACAGCGCTCCCTGACCATCTCTGGGCTC 240
QY 241 CAGCTGAGGAGGAGGCTGATATATCTGTTGTTATATACACAGCAGTACCTTTGTTA 300
DB 241 CAACCTGAGGATGAGGCTGATATATTTGCGCCTCATATGAGGAGCAGTAACATCGTAATA 300
QY 301 TTCGGAAGAGGAGCCCGGTTCCACGCTCTAGGT 333
DB 301 TTCGCGGAGGAGCAAGATTGACCGTCTAGGT 333
```

```
RESULT 11
ACC85452
ID ACC85452 standard; DNA; 330 BP.
XX ACC85452;
XX ACC85452;
XX 29-SEP-2003 (first entry)
XX Human glycoprotein VI antibody IC3 variable light chain DNA.
XX Human; antibody; glycoprotein VI; GPVI; 10B12; IC3; variable heavy;
XX variable light; CDR; platelet aggregation; cardiant; thrombolytic;
XX cerebroprotective; antisickling; vasotropic; cardiovascular disease;
XX Gene; ds.
XX Homo sapiens.
XX WO2003054020-A2.
XX 03-JUL-2003.
XX 18-DEC-2002; 2002WO-GB005755.
XX 20-DEC-2001; 2001GB-00030543.
XX (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
XX Smethurst PA, Ouwehand WH, Farndale RW;
XX WPI; 2003-559127/52.
XX P-PSDB; ABR63614.
XX New specific binding member binding human glycoprotein VI (GPVI) and
XX comprising an antibody VH domain and/or an antibody VL domain, useful for
XX the manufacture of a medicament for treating a disorder, e.g., thrombosis
XX or stroke.
XX Disclosure; Page 88; 127pp; English.
XX The present invention relates to a specific binding member which binds
XX human glycoprotein VI (GPVI), comprising an antibody VH domain and/or an
XX antibody VL domain. The antibody VH domain comprises 10B12 VH domain, IC3
XX VH domain or a VH domain comprising a VH CDR3 or optionally one or more
XX VH CDR's. The antibody VL domain comprises 10B12 VL domain, IC3 VL domain
XX and a VL domain comprising one or more VL CDRs. The specific binding
XX member is useful for the manufacture of a medicament for treating a
XX disease or disorder comprising cardiovascular conditions, thrombosis,
XX stroke, intermittent claudication, conditions with disseminated
XX intravascular coagulation, thrombocytopenic purpura, haemolytic uraemic
XX syndrome, damage to blood vessel wall resulting from surgery or therapy,
XX collagen-induced inflammation, homozygous sickle disease, kidney damage,
XX by platelet and fibrin disposition on the glomerular membrane or micro-
XX angiopathic vasculitides. The present sequence is a coding sequence of an
XX antibody domain shown in the exemplification of the invention
XX Sequence 330 BP; 70 A; 100 C; 85 G; 75 T; 0 U; 0 Other;

Query Match 78.9%; Score 262.8; DB 8; Length 330;
Best Local Similarity 87.3%; Pred. No. 2.2e-72;
Matches 288; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 1 CAGTCTGCCCGACTCAGCCCTCCCTCTGTGCTGGTCTCTGACAGTGGTCAACCATC 60
DB 1 CAGTCTGGTGGTGGAGCGCGGCTCCATGCTCTGGCGCCCGCAGGACAGAGGTCACCATC 60
QY 61 TCCTGCATGGAACACGAGATGACGTTGGTGGTTATTAATACTATGCTCTCTGTATCAACAC 120
DB 61 TCCTGCATGGAACACGAGATGACGTTGGTGGTTATTAATACTATGCTCTCTGTATCAACAC 120
QY 121 CACCCAGGCAAGCCCCCAACTCATGTTATGATGCTGCTAGCGGCTCAGGGGTC 180
```

Db 121 CACCAGCAAAAGCCCAAACTCATGCTTTTGGAGTCAGTCATCGCCGCTCAGGGGTT 180
Qy 181 TCTGATGCTTCTCTGGCTCCCAAGTCTGGCAACACGGCTCCCTGACCATCTCTGGGCTC 240
Db 181 TCTGATGCTTCTCTGGCTCCCAAGTCTGGCAACACGGCTCCCTGACCATCTCTGGGCTC 240
Qy 241 CAGGCTGAGGACGAGGCTGATTTACTTGTGTTTCATATACCAACAGTAGCATTCTTTA 300
Db 241 CAGGCTGAGGACGAGGCTGATTTACTTGTGTTTCATATACCAACAGTAGCATTCTTTA 300
Qy 301 TTCCGAAGAGGACCCCGGTTACCGTCTTA 330
Db 301 TTCCGGGAGGAGGACCAAGGTACCGTCTTA 330

RESULT 12
AAF58706
ID AAF58706 standard; DNA; 327 BP.
XX
AC AAF58706;
XX
Dt 30-APR-2001 (first entry)
XX
DE Huntingtin minimal sfv binding region coding sequence #2.
XX

XX Neurological disorder; Huntington's disease; Alzheimer's disease;
KW Parkinson's disease; prion disease; frontotemporal dementia;
KW amyotrophic lateral sclerosis; spinal and bulbar muscular atrophy;
KW dentatorubral-pallidoluysian atrophy; spinocerebellar ataxia type 1; SCA2;
KW SCA3; SCA4; SCA5; SCA6; SCA7; protein accumulation; intrabody; ds.
XX
OS Unidentified.
XX

PN WO200106989-A2.
XX
PD 01-FEB-2001.
XX
PF 24-JUL-2000; 2000WO-US020131.
XX
PR 27-JUL-1999; 99US-0146047P.
XX
P3 21-JUL-2000; 2000US-00620955.
XX

PA (HUST)/ HUSTON J S.
FA (MESS)/ MESSER A.
PA (LECE)/ LECERF J.
XX
Pi Huston JS, Messer A, Lecerf J;
XX
DR WPI: 2001-182700/18.
DR P-PSDB; AAB59602.
XX

XX Inhibiting intracellular polypeptide accumulation, useful for treating
XX neurological disorders, e.g. Alzheimer's disease, comprises contacting
XX the polypeptide with a specific intrabody.
XX
PS Disclosure; Page 93; 108pp; English.
XX

XX The present invention describes a method for inhibiting the formation of
XX aggregates of certain proteins, involving contacting the protein with a
XX binding molecule known as an intrabody. Proteins to be bound include
XX those associated with neurological disorders, and so the method can be
XX used in the prevention of diseases such as Alzheimer's, Parkinson's and
XX Huntington's diseases, prion disease, frontotemporal dementia,
XX amyotrophic lateral sclerosis, spinal and bulbar muscular atrophy,
XX dentatorubal-pallidoluysian atrophy, spinocerebellar ataxia type 1
XX (SCA1), SCA2, SCA3, SCA4, SCA5, SCA6 and SCA7
XX
SQ Sequence 327 BP; 64 A; 102 C; 79 G; 82 T; 0 U; 0 Other;

Query Match 74.6%; Score 248.4; DB 4; Length 327;
Best Local Similarity 86.7%; Pred. No. 7.4e-69;
Matches 286; Conservative 0; Mismatches 41; Indels 3; Gaps 1;

Qy 1 CAGTCTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCTGGACAGTCGGTCACCATC 60
Db 1 CAGTCTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCTGGACAGTCGGTCACCATC 60
Qy 61 TCTGCACTGGACAGGACGATGACGTTGGTGTATTAACATGATCTCTGTTACCAACAC 120
Db 61 TCTGCACTGGACAGGACGATGACGTTGGTGTATTAACATGATCTCTGTTACCAACAG 120
Qy 121 CACCCAGGCAAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGCTCAGGGGTC 180
Db 121 TATCCAGGCAAGGCCCCCAAACTCCTTTATTTATGATGTCAGTAATCGGCCCTCAGGGATT 180
Qy 181 TCTGATGCTTCTCTGGCTCCCAAGTCTGGCAACACGGCTCCCTGACCATCTCTGGGCTC 240
Db 181 TCTATGCTTCTCTGGCTCCCAAGTCTGGCAACACGGCTCCCTGACCATCTCTGGGCTC 240
Qy 241 CAGGCTGAGGACGAGGCTGATTTACTTACTTGTTCATATACCAACAGTAGCATTCTTTA 300
Db 241 CAGGCTGAGGACGAGGCTGATTTACTTACTTGTTCATATACCAACAGTAGCATTCTTTA 300
Qy 301 TTCCGAAGAGGACCCCGGTTGACCGTCTTA 330
Db 298 TTCCGGGAGGAGGACCAAGGTACCGTCTTA 327

RESULT 13
AAD46293
ID AAD46293 standard; DNA; 330 BP.
XX
AC AAD46293;
XX
Dt 27-DEC-2002 (first entry)
XX
DE Human KDR (VEGFR-2) Fab light chain (VL) DNA from D1H4 clone.
XX

XX Human; tumour; vascular endothelial growth factor receptor; metastasis;
KW epidermal growth factor receptor; non-small cell lung carcinoma; NSCLC;
KW breast; VEGFR; heart; EGFR; therapy; invasiveness; light chain; gene; VL;
XX ds.
XX Homo sapiens.

OS
PH Key Location/Qualifiers
FT CDS 1..330
FT /*tag= a
FT /product= "Human KDR (VEGFR-2) Fab light chain (VL)
FT protein"
FT /note= "CDS does not include start and stop codon"
FT /partial
XX

PN WO200270008-A1.
XX
PD 12-SEP-2002.
XX
PP 04-MAR-2002; 2002WO-US006762.
XX
PR 02-MAR-2001; 2001US-00798689.
XX

XX (IMCL-) IMCLONE SYSTEMS INC.
PA (ROCK/) ROCKWELL P.
PA (GOLD/) GOLDSTEIN N I.
XX
XX WPI: 2002-691738/74.
DR P-PSDB; AAE28872.

XX Inhibiting tumor growth in humans involves administering vascular
XX endothelial growth factor receptor antagonists in combination with
XX radiation, chemotherapeutic agents, or epidermal growth factor receptor
XX antagonists.

XX Example 12; Page 125; 151pp; English.
XX
CC The invention relates to a method of inhibiting tumour growth which


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XX 04-MAR-2002; 2002US-00091300.
PF
XX 10-FEB-1994; 94US-00196041.
XX 20-OCT-1994; 94US-00326552.
PR 07-JUN-1995; 95US-00476533.
PR 03-SEP-1996; 96US-00706804.
PR 07-JAN-1997; 97US-00779450.
PR 10-NOV-1997; 97US-00967113.
PR 22-SEP-1999; 99US-00401163.
PR 02-MAR-2001; 2001US-00798689.
XX (ROCK/) ROCKWELL P.
PA (GOLD/) GOLDSTEIN N I.
XX
XX Rockwell P, Goldstein NI;
XX
XX WPI; 2003-801265/75.
DR P-PSDE; ADD24422.
XX
XX Inhibiting tumor growth by administering to a human a vascular
PT endothelial growth factor receptor (VEGFR) antagonist and epidermal
PT growth factor receptor (EGFR) antagonist.
XX
XX Example 12; SEQ ID NO 28; 90pp; English.
XX
XX The invention relates to a method of inhibiting tumour growth comprising
CC administering to a human a vascular endothelial growth factor receptor
CC (VEGFR) antagonist and epidermal growth factor receptor (EGFR)
CC antagonist. The method is useful for inhibiting tumour growth. The
CC present sequence is used in the exemplification of the invention.
XX
XX Sequence 330 BP; 73 A; 104 C; 72 G; 81 T; 0 U; 0 Other;
SQ
Query Match 73.2%; Score 243.6; DB 9; Length 330;
Rest Local Similarity 83.6%; Pred No. 2.4e-66;
Matches 276; Conservative 0; Mismatches 54; Indels 0; Gaps 0;
QY 1 CAGTCTGCCCGACTCAGCTCCCTCTGTCTGTGGTCTCTCGGACAGTCGGTCCACCATC 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 CAGTCTGCCCGACTCAGCTCCCTCTGTCTGTGGTCTCTCGGACAGTCGGTCCACCATC 60
QY 61 TCCTGCACTGGRACCCAGCGATGACGTGGTGGTTATATATATATCTCTCTGGTACCAAC 120
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
61 TCCTGCGCTGGAAACCCACCCTGATCTTACATATATATGACCTGTCTCTGGTACCAAC 120
QY 121 CACCCAGGCCAAGCCGCCAACTCATGATTTATGATGTGGCTAAGCGGCGCTCAGGGGTC 180
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
121 CACCCAGGCCAAGCCGCCAACTCTGTGATTTATGCGGCAATAAGCGGCGCTCAGGAGTT 180
QY 181 TCTGATCGCTTCTCTGGTCCAGCTGGGACACACGGGCTCCGTGACCATCTCTGGGCTC 240
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
181 TCTAATCGCTTCTCTGGTCCAGCTGGGACACACGGGCTCCGTGACCAATCTCTGGACTC 240
QY 241 CAGGCTGAGGACGAGGCTGATTATTAATCTGTGTTCATATACACCACTAGCACTTTGTTA 300
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
241 CAGGCTGAGGACGAGGCTGATTATTAATCTGTGTTCATATACCACTAGCACTTTTATGTC 300
QY 301 TTCGGAAGGAGGACCGGTTGACCGTCCTA 330
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
301 TTCGGAACCTGGGACCAAGGTCACCGTCCTA 330

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Search completed: June 19, 2004, 03:30:41
Job time : 279 secs

61	QY	TCCTGCAC	TGGAAAC	CAGCGAT	GACGTT	GGTGGT	TATTAAC	TATGTCT	CCGTGGT	TACCAAC	120
	DB										
61	QY	TCCTGCAC	TGGAAAC	CAGCGAT	GACGTT	GGTGGT	TATTAAC	TATGTCT	CCGTGGT	TACCAAC	120
	DB										
121	QY	CACCCAGG	CAAGCCC	CAAACTC	ATGATT	TATGAT	TCTCGT	AAGCGG	CCCTC	AGGGGTC	180
	DB										
121	QY	CACCCAGG	CAAGCCC	CAAACTC	ATGATT	TATGAT	TCTCGT	AAGCGG	CCCTC	AGGGGTC	180
	DB										
181	QY	TCTGATCG	CTTCTCG	GCTCCAA	GTCGCA	ACGGCCT	CCCTG	GACCAT	CTCTCGG	GCTC	240
	DB										
191	QY	CCATCGCT	TCTCAG	GCTCCAA	GTCGCA	ACGGCCT	CCCTG	GACCAT	CTCTCGG	GCTC	240
	DB										
241	QY	CAGCTGAG	GAGGAGG	CTGATT	TACTGTT	GTGATAT	TACAC	CAGTAGG	CATCTTG	TGTA	300
	DB										
241	QY	CAGCTGAG	GAGGAGG	CTGATT	TACTG	CAGCTC	ACTTAC	ACGCAGAG	TCACTCTG	TGATC	300
	DB										
301	QY	TTCCGAA	GAGGAGC	CCCGGTT	GA	CCGCTC	TAGGT				333
	DB										
301	QY	TTCCGCG	GAGGAGC	CAAA	GCTGA	CCGCTC	TAGGT				333
	DB										

```

1  RESULT 2
2  US-08-958-201-11
3  ; Sequence 11, Application US/08958201
4  ; Patent No. 5977319
5  ; GENERAL INFORMATION:
6  ; APPLICANT: Pope, Anthony R
7  ; APPLICANT: Pritchard, Kevin J
8  ; APPLICANT: Williams, Andrew J
9  ; APPLICANT: Johnson, Kevin S
10 ; TITLE OF INVENTION: Specific binding members for estradiol;
11 ; TITLE OF INVENTION: materials and methods
12 ; NUMBER OF SEQUENCES: 23
13 ; CORRESPONDENCE ADDRESS:
14 ; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
15 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
16 ; CITY: Chicago
17 ; STATE: Illinois
18 ; COUNTRY: USA
19 ; ZIP: 60606-6402
20 ; COMPUTER READABLE FORM:
21 ; MEDIUM TYPE: Floppy disk
22 ; COMPUTER: IBM PC compatible
23 ; OPERATING SYSTEM: PC-DOS/MS-DOS
24 ; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
25 ; CURRENT APPLICATION DATA:
26 ; APPLICATION NUMBER: US/08/958,201
27 ; FILING DATE:
28 ; PRIOR APPLICATION DATA:
29 ; APPLICATION NUMBER: US 60/028,897
30 ; FILING DATE: 21-OCT-1996
31 ; INFORMATION FOR SEQ ID NO: 11:
32 ; SEQUENCE CHARACTERISTICS:
33 ; LENGTH: 333 base pairs
34 ; TYPE: nucleic acid
35 ; STRANDEDNESS: double
36 ; TOPOLOGY: linear
37 ; IMMEDIATE SOURCE:
38 ; CLONE: D12 (light chain)
39 ; FEATURE:
40 ; NAME/KEY: CDS
41 ; LOCATION: 1..333
42 US-08-958-201-11

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Query Match      82.2%; Score 273.8; DB 2; Length 333;
Best Local Similarity 88.9%; Pred. No. 2e-77;
Matches 296; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 1 CAGTCTCCCGACTCAGCCTCCCTCTGTCTGTGGGTCTCTGGACAGTCGTCACCATC 60
Db 1 CAGTCTCTCTGACTCAGCCTGCGCTGTGTGTGTGGGTCTCTGGACAGTCGTCACCATC 60

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COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US/08/652.816A
PRIOR APPLICATION DATA:
FILING DATE: 02-DEC-1991
APPLICATION NUMBER: GB 9125579.4
PRIOR APPLICATION DATA:
FILING DATE: 02-DEC-1991
APPLICATION NUMBER: GB 9125579.8
PRIOR APPLICATION DATA:
FILING DATE: 02-DEC-1991
APPLICATION NUMBER: GB 9206318.9
PRIOR APPLICATION DATA:
FILING DATE: 24-MAR-1992
APPLICATION NUMBER: GB 9206372.6
PRIOR APPLICATION DATA:
FILING DATE: 23-SEP-1992
APPLICATION NUMBER: GB 9525004.9
PRIOR APPLICATION DATA:
FILING DATE: 07-DEC-1995
APPLICATION NUMBER: GB 9610824.6
PRIOR APPLICATION DATA:
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: PCT/GB92/02240
PRIOR APPLICATION DATA:
FILING DATE: 02-DEC-1992
APPLICATION NUMBER: US 08/244,597
FILING DATE: 01-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/33308
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 27:
LENGTH: 333 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-652-816A-27

Query Match 57.7%; Score 192; DB 2; Length 333;
Best Local Similarity 77.4%; Pred. No. 1.7e-51;
Matches 260; Conservative 0; Mismatches 70; Indels 6; Gaps 2;

QY 1 CAGTCTCCCGACTCAGCCTCCCTCTGTCTGTGGGTCTCTGTGACACAGTCCGTCACCATC 60
DB 1 CAGTCTGTGTGACGAGCGCCCTCAGTGTCTGTGGGCCCCCAGGACAGAGGTCAACATT 60
QY 61 TCCTGCTGGAACACGAGGATGACGTGTGGTGTATTAATCTCTGTGTACCAAC 120
DB 61 TCCTGCTGTGAGACACCCCAACAT---TGGGAATAATTAATGTCTCTGTGTACCAACAG 117
QY 121 CACCCAGGAAAGCCCCCAACTCATGATTTATGATCTGCTAAGCGGGCTCAGGGGTC 180
DB 118 CACCCAGGAAAGCCCCCAACTCATGATTTATGATGTAGTAAGCGCCCTCAGGGGTC 177
QY 181 TCTGATCGTTCTCTGTGCTCAAGTCTGGCAACACGCGCTCCCTGACATCTCTGTGGGTC 240
DB 178 CTTGACCGATTCTCTGTGCTCAAGTCTGGCAACTGCGCACTCCCTGACATCAGTGGGTC 237
QY 241 CAGGCTGAGGACGAGGCTGATTATTACTGTGTTTCAT---ATACCAACAGTAGCACTTTG 297
DB 238 CAGTCTGAGGATGAGGCTGATTATTACTGTGACATGGGATGACGCTGAGTGAATTT 297
QY 298 TTATTCGGAAGAGGACCCCGTTGACCGTCTAGGT 333
DB 298 CTCTTCGGAACCTGGACCAAGCTGAGATCAACAGT 333

RESULT 4
US-09-240-274-138
Sequence 138, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 138
LENGTH: 312
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain S01
US-09-240-274-138

Query Match 62.7%; Score 208.8; DB 3; Length 312;
Best Local Similarity 83.6%; Pred. No. 8e-57;
Matches 266; Conservative 0; Mismatches 37; Indels 15; Gaps 2;

QY 13 ACTGAGCTCCCTCTGTGTCTGGTCTCTGTGACAGTGGTCCACATCTCTCTGCACTGA 72
DB 10 ACTGAGCTCCCTCTGTGTCTGGTCTCTGTGACAGTGGTCCACATCTCTCTGCACTGA 65
QY 73 ACCAGGATGAGTGTGGTGTATTAATGATCTCTGTGTACCAACACACCCAGGAAA 132
DB 66 -----TGATGTGGGAATTAATACCTGTCTCTGTGTACCAACAGTACCCAGCAAG 117
QY 133 GCCCCCAACTCATGATTTATGATCTGCTAAGCGGCTCAGGGTCTCTGATCGCTTC 192
DB 118 GCCCCCAACTCATGATTTATGAGGCTAGTACGCGCCCTCAGGGGTTTCTAGTCTGCTTC 177
QY 193 TCTGGCTCCCAAGTCTGGCAACAGGCTCCCTGACCATCTCTGGGCTCCAGGCTGAGGAC 252
DB 178 TCTGGCTCCAGGCTGGCAACAGGCTCCCTGACCATCTCTGGGCTCCAGGCTGAGGAC 237
QY 253 GAGGCTGATTAATGATGTTTATATACATATACACAGTAGCACTTTGTTATGGAAGAGG 312
DB 238 GAGGCTGATTAATGATGTTTATATGCTCATATGCAATTAGTAGCA---GGATTTTGGGCGAGGG 294
QY 313 ACCCGTTGACCGTCTTA 330
DB 295 ACCNAGCTGACCGTCTTA 312

RESULT 5
US-08-652-816A-27

Sequence 27, Application US/08652816A
Patent No. 5872215
GENERAL INFORMATION:
APPLICANT: Osbourn, JK
APPLICANT: Allen, DJ
APPLICANT: McCafferty, JG
TITLE OF INVENTION: Specific binding members, materials and
TITLE OF INVENTION: methods.
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America

RESULT 6
US-09-240-274-132
; Sequence 132, Application US/09240274
; Patent No. 6259455
; GENERAL INFORMATION:
; APPLICANT: Sigel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 132
; LENGTH: 330
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 001
US-09-240-274-132

Query Match 53.6%; Score 178.6; DB 3; Length 330;
Best Local Similarity 74.5%; Pred. No. 3.1e-47;
Matches 239; Conservative 0; Mismatches 79; Indels 3; Gaps 1;

QY 13 ACTCAGCTCCCTCTGTGCTGGTCTCTGGGACAGTCGCTCACCATCTCTGCCTGGA 72
DB 10 ACGCAGCGCCCTCAGTGTCTGGGCCCCAGGCGGTACCATCTCTGCCTGG 69
QY 73 ACACGAGTACGCTGTGGTGTATATATGTCTCTGGTACCAACACCCAGGAAA 132
DB 70 AGCAGCTCCCAACTCGGGGACCTTATGTGTACATCTGTGTACCTGCTACGAGGTTTCCAGGA 129
QY 133 GCCCCAACTCATGATTTATGCTGCTAAGCGGCTCAGGGGTCTGTGATCGCTTC 192
DB 130 GCCCCAACTCATGCTCTACATGCAATCGGCGCTCAGGGGTCTGTGATCGCTTC 189
QY 193 TCTGGTCTCAAGTCTGGCAACAGGCTCTCTGACCATCTCTGGGTTCCAGGCTGAGGAC 252
DB 190 TCTGGTCTCAAGTCTGGCACTCAGGCTCTCTGACCATCTCTGGGTTCCAGGCTGAGGAT 249
QY 253 GAGGCTGATTTACTGTTCTTATATACATACACAG---TAGCATTCTTGTATTGGAAGA 309
DB 250 GAGGCTGATTTACTGCTCCAGTCTCTATGACAGCAGCTGAGTGAAGAGGTTTCCGCGGA 309
QY 310 GGGACCGGTTGACCGCTCTA 330
DB 310 GGGACCAAGCTGACCGCTCTA 330

RESULT 7
US-08-199-911-1
; Sequence 1, Application US/08199911
; Patent No. 5495002
; GENERAL INFORMATION:
; APPLICANT: Kohnin, Barry J.
; APPLICANT: Haspel, Martin V.
; TITLE OF INVENTION: Tumor Associated Monoclonal Antibody
; TITLE OF INVENTION: 123AV16
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESS: AKZO NOBEL
; STREET: 1330 Piccard Drive
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850

Query Match 52.9%; Score 176.2; DB 1; Length 330;
Best Local Similarity 74.8%; Pred. No. 1.8e-46;
Matches 249; Conservative 0; Mismatches 78; Indels 6; Gaps 2;

QY 1 CAGTCTGCCCGACATCAGCTCCCTCTGTGTGGTCTCTGTGACAGTCTGGTACCATC 60
DB 1 CAGTCTGCCGTTGACGACGCGCCCTCAGTATCTGGGCCCCAGGACAGAGGTACCATC 60
QY 61 TCCTGCTCTGGAACCAAGCTCCCAACAT---TGGATATATTTTGTATCTCTGGTACCAAC 120
DB 61 TCCTGCTCTGGAACCAAGCTCCCAACAT---TGGATATATTTTGTATCTCTGGTACCAAC 117
QY 121 CACCAGGCAAGGCCCCCAACTATGATTTATGCTGCTAGCGGGCTCTCAGGGGTC 180

Db	118	TTCCAGGGACAGCCGCCAAACTCTCTATTATGACAATAATAGAGGACCCCTCAGGGTT	177
Qy	181	TCGTGATCGTTCTCTGGCTCCAAAGTCGGGAAACGGCTCCCTGACCATCTCTGGGTC	240
Db	178	CCTGACCAATTCTCTGGCTCCAAAGTCGGGAAACGGCTCCCTGACCATCTCTGGGTC	237
Qy	241	CAGGCTGAGGACGAGGCTGATTATTACTGTGTTTCAT---ATACAAACCAGTAGCACTTTG	297
Db	238	CAGACTGGGACGAGGCCGATTATTACTGCGGACATGGGATACAGACTGGCGCTGGT	297
Qy	298	TTATTCCGAAGAGGGAACCCGGTTGACGTCCTTA	330
Db	298	GTGTTCGGCGAGGGAACCAAGCTACCGTCTTA	330

RESULT 8
 US-08-477-553A-43
 ; Sequence 43, Application US/08477553A
 ; Patent No. 5919910
 ; GENERAL INFORMATION:
 ; APPLICANT: HUGHES-JONES, Nevin C
 ; TITLE OF INVENTION: MONOCLONAL ANTIBODIES
 ; NUMBER OF SEQUENCES: 55
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSES: Burns, Doane, Swecker & Mathis
 ; STREET: P.O. Box 1404
 ; CITY: Alexandria
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22313-1404
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/477,553A
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/856,034
 ; FILING DATE: 23-JUNE-1992
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: GB 8925590.5
 ; FILING DATE: 13-NOV-1989
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Meuth, Donna M.
 ; REGISTRATION NUMBER: 36,607
 ; REFERENCE/DOCKET NUMBER: 007330-032
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 836-6620
 ; TELEFAX: (703) 836-2021
 ; INFORMATION FOR SEQ ID NO: 43:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 333 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 US-08-477-553A-43

QY 121 CACCAGGCAAGCCCCCAAACTCATGTTTATGATGTCGTAAGCGGGCCTCAGGGGTC 180
 |||||
 Db 118 CTCGAGGACAGCCCCCAAACTCCTCATTTATGACAATAATAAGCGACCCCTCAGGGATT 177
 |||||
 QY 181 TCGATCGCTTCTTGGCTCCAAGTCGGCAACACAGCGCTCCCTGACCATCTCTGGGGTC 240
 |||||
 Db 178 CCGACCGATTCTCTGGCTCAAAGTCGGCACGTCAGCCACCTTGGGCATCACCAGACTC 237
 |||||
 QY 241 CAGGCTGAGGACGAGGCTGATTATTACTGTGTTTCAT---ATACAAACGAGTAGCACTTTG 297
 |||||
 Db 238 CCGACTGGGACAGAGCCGATTATTACTCGCAACATGGGATAGCAGCCTGAGTGCTGTG 297
 |||||
 QY 298 TTATTGGGAAGAGGAGCCCGGTTGACCGTCTTAGGT 333
 |||||
 Db 298 GTGTCGGCGAGGGACCAAGCTGACCGTCTTAAGT 333
 |||||

RESULT 9
 US-09-240-274-134
 ; Sequence 134, Application US/09240274
 ; Patent No. 6255455
 ; GENERAL INFORMATION:
 ; APPLICANT: Siegel, Donald L.
 ; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
 ; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
 ; FILE REFERENCE: 09596-42U2
 ; CURRENT APPLICATION NUMBER: US/09/240,274
 ; CURRENT FILING DATE: 1999-01-29
 ; EARLIER APPLICATION NUMBER: 60/081,380
 ; EARLIER FILING DATE: 1998-04-10
 ; EARLIER APPLICATION NUMBER: 60/028,550
 ; EARLIER FILING DATE: 1996-10-11
 ; NUMBER OF SEQ ID NOS: 224
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 134
 ; LENGTH: 330
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: anti-Rh(D) chain O03
 US-09-240-274-134

RESULT 10

Search completed: June 19, 2004, 04:31:43
Job time : 64 secs

QY 61 TCCTGCACTGAAACAGCGATGACGTTGGTGGTTATTAACATATGTCCTGTGACCAACAC 120
DB 61 TCCTGCACTGAAACAGCGATGACGTTGGTGGTTATTAACATATGTCCTGTGACCAACAA 120
QY 121 CACCCAGGCAAGCCGCCAACTCANGATTTATGATGTCGCTAAGCGGGCTCAGGGGTC 180
DB 121 CACCCAGGCAAGCCGCCAACTCANGATTTATGATGTCGCTAAGCGGGCTCAGGGGTT 180
QY 181 TCTGATCGCTTCTTGGCTCCAGTCTCGCAACACGGCTCCCTGACCATCTCTGGGCTC 240
DB 181 TCTAATCGCTTCTTGGCTCCAGTCTCGCAACACGGCTCCCTGACCATCTCTGGGCTC 240
QY 241 CAGCTGAGGACGAGGCTGATTTACTGTTTATATACAAACAGGAGGACATTTGTTA 300
DB 241 CAGCTGAGGACGAGGCTGATTTACTGTTTATATACAAACAGGAGGACATTTGTTA 300
QY 301 TTCGGAAGGAGGACCGGCTTACCGTCTCTAG 331
DB 301 TTCGGAAGGAGGACCGGCTTACCGTCTCTAG 331

RESULT 2

US-10-172-118-200
; Sequence 200, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10172.118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 200
; LENGTH: 331
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AJ249377
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-200

Query Match 85.5%; Score 284.6; DB 13; Length 331;
Best Local Similarity 91.2%; Pred. No. 4.4e-87;
Matches 302; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 1 CAGTCTGCCCGACTCAGCCCTCCCTCTGTCGTGGTCTCTCTGACAGAGTGGTCAACATC 60
DB 1 CAGTCTGCCCGACTCAGCCCTCCCTCTGTCGTGGTCTCTCTGACAGAGTGGTCAACATC 60
QY 61 TCCTGCACTGAAACAGCGATGACGTTGGTGGTTATTAACATATGTCCTGTGACCAACAC 120
DB 61 TCCTGCACTGAAACAGCGATGACGTTGGTGGTTATTAACATATGTCCTGTGACCAACAA 120
QY 121 CACCCAGGCAAGCCGCCAACTCATGATTTATGATGTCGCTAAGCGGGCTCAGGGGTC 180
DB 121 CACCCAGGCAAGCCGCCAACTCATGATTTATGATGTCGCTAAGCGGGCTCAGGGGTT 180
QY 181 TCTGATCGCTTCTTGGCTCCAGTCTGGCAACACGGCTCCCTGACCATCTCTGGGCTC 240
DB 181 TCTAATCGCTTCTTGGCTCCAGTCTGGCAACACGGCTCCCTGACCATCTCTGGGCTC 240
QY 241 CAGCTGAGGACGAGGCTGATTTACTGTTTATATACAAACAGGAGGACATTTGTTA 300
DB 241 CAGCTGAGGACGAGGCTGATTTACTGTTTATATACAAACAGGAGGACATTTGTTA 300

DB 241 CAGGCTGAGACGAGGCTGATTATTACTGCAGCTCATATACAAGCAGCAGCACTCGGGTG 300
QY 301 TTCGGAGAGGAGCCCGGTTGACCGTCTCTAG 331
DB 301 TTCGGAGAGGAGCCCGGTTGACCGTCTCTAG 331
RESULT 3
US-10-399-518-96
; Sequence 96, Application US/10399518
; Publication No. US20040091475A1
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, MASAYUKI
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: YABUTA, NAOHITO
; APPLICANT: TSUNODA, HIROYUKI
; APPLICANT: ORITA, TETSURO
; TITLE OF INVENTION: DEGRADED TPO AGONIST ANTIBODY
; FILE REFERENCE: 065678/0111
; CURRENT APPLICATION NUMBER: US/10/399,518
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: PCT/JP01/03288
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: JP 2001-277314
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: JP 2000-321821
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 96
; LENGTH: 330
; TYPE: DNA
; ORGANISM: Mus sp.
US-10-399-518-96

Query Match 82.8%; Score 275.8; DB 17; Length 330;
Best Local Similarity 90.2%; Pred. No. 4.6e-84;
Matches 295; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 4 TCTGCCCGGACTCAGGCTCCCTCTGTCGTGGTCTCTCTGGACAGTCGGTCAACATCTCC 63
DB 4 TATGCTGACTCAGCCACCTCGGTGTCAGGGTCTCTCTGGACAGTCGATCACCATCTCC 63
QY 64 TGCACCTGGAACAGCGATGACGTTGGTGGTTATAACTATGTCCTCTGGTACCAACACAC 123
DB 64 TGCACCTGGAACAGCGATGACGTTGGTGGTTATAACTATGTCCTCTGGTACCAACACAC 123
QY 124 CCAGGCAAGCCGCCAACTCATGATTTATGATGTCGCTAAGCGGCTCAGGGGTTCT 183
DB 124 CCAGGCAAGCCGCCAACTCATGATTTATGATGTCGCTAAGCGGCTCAGGGGTTCT 183
QY 184 GATCGCTTCTCTGGCTCCAAAGTCTGGCAACACGGGCTCCCTGACCATCTCTGGGTTCCAG 243
DB 184 AATGCTTCTCTGGCTCCAAAGTCTGGCAACACGGGCTCCCTGACCATCTCTGGGTTCCAG 243
QY 244 GCTGAGGACGAGGCTGATTTACTGTTGTTTATATACAGCAGTAGCACTTTGTTATTC 303
DB 244 GCTGAGGACGAGGCTGATTTACTGTTGTTTATATACAGCAGTAGCACTTTGTTATTC 303
QY 304 GGAAGAGGAGCCCGGTTGACCGTCTCTA 330
DB 304 GCGGAGGAGGAGCCAGCTGACCGTCTCTA 330

RESULT 4

US-10-663-244-86
; Sequence 86, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS

```
/ FILE REFERENCE: 10280-063001
/ CURRENT APPLICATION NUMBER: US/10/663,244
/ CURRENT FILING DATE: 2003-09-15
/ PRIOR APPLICATION NUMBER: US 60/410,758
/ PRIOR FILING DATE: 2002-09-13
/ PRIOR APPLICATION NUMBER: US 60/469,123
/ PRIOR FILING DATE: 2003-05-09
/ NUMBER OF SEQ ID NOS: 165
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 86
/ LENGTH: 319
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetically generated oligonucleotide
US-10-663-244-86

Query Match      81.4%; Score 271; DB 17; Length 319;
Best Local Similarity 90.6%; Pred. No. 2e-B2;
Matches 289; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

Qy 12 GACTCAGCTCCCTCTGTCGTCGGTCTCCCTGGACAGTCGGTACCAATCTCTGCACTGG 71
Db 1 GACTCAGCTCCCTCTGTCGTCGGTCTCCCTGGACAGTCGGTACCAATCTCTGCACTGG 60
Qy 72 AACCAGCGATCAGCTGGTGGTTAATGCTATGCTCTCTGGTACCAACACACCCAGGCAA 131
Db 61 AACCAGCGATCAGCTGGTGGTTAATGCTATGCTCTCTGGTACCAACACACCCAGGCAA 120
Qy 132 AGCCCCAACTCATGATTTATGATGTCGCTAAGCGGCCCTCAGGGGTCTCTGATCGCTT 191
Db 121 AGCCCCAACTCATGATTTATGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 180
Qy 192 CTCTGGCTCCAGTCTGTCACACAGCGCTCTCTGACCATCTCTGGCTCCAGGCTGAGGA 251
Db 181 CTCTGGCTCCAGTCTGTCACACAGCGCTCTCTGACCATCTCTGGCTCCAGGCTGAGGA 240
Qy 252 CGAGCTGATTTACTTCTGTCATATACACACAGTACGACTTGTATTTCGGAAGAGG 311
Db 241 CGAGCTGATTTACTTCTGTCATATACACAGTACGACTTGTATTTCGGAAGAGG 300
Qy 312 GACCGGTTGACCGTCTTA 330
Db 301 GACCGGTTGACCGTCTTA 319

RESULT 5
US-10-029-386-14141/c
/ Sequence 14141, Application US/10029386
/ Publication No. US20030194704A1
/ GENERAL INFORMATION:
/ APPLICANT: Penn, Sharon G.
/ APPLICANT: Rank, David K.
/ APPLICANT: Hanzel, David K.
/ TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
/ TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
/ FILE REFERENCE: AEWICA-X-2
/ CURRENT APPLICATION NUMBER: US/10/029,386
/ CURRENT FILING DATE: 2001-12-20
/ NUMBER OF SEQ ID NOS: 34288
/ SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
/ SEQ ID NO 14141
/ LENGTH: 294
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: MAP TO CHR22 155.0
/ OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.52
/ OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 5.6
/ OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
/ OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.53
/ OTHER INFORMATION: NT HIT: Z85032.1, EVALUE 0.00e+00
/ OTHER INFORMATION: SWISSPROT HIT: P01705, EVALUE 3.00e-47

/ OTHER INFORMATION: EST_HUMAN HIT: BG754419.1, EVALUE 0.00e+00
US-10-029-386-14141

Query Match      73.6%; Score 245.2; DB 15; Length 294;
Best Local Similarity 91.8%; Pred. No. 1.4e-73;
Matches 259; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Qy 1 CAGTCTGCCCGGACTCAGCTCCCTCTGTCGTCGGGTCTCTCTGGACAGTCGGTCAACATC 60
Db 283 CAGTCTGCCCGGACTCAGCTCCCTCTGTCGTCGGGTCTCTCTGGACAGTCGGTCAACATC 224
Qy 61 TCCTGCACCTGGAAACAGCGATGAGCTTGGTGGTTTAACTATGTCCTCTGGTACCAACAC 120
Db 223 TCCTGCACCTGGAAACAGCGATGAGCTTGGTGGTTTAACTATGTCCTCTGGTACCAACAG 164
Qy 121 CACCCAGGCAAGCCGCCCAAACTCATGATTTATGAGGCGAGTAAGCGGCCCTCAGGGGTC 180
Db 163 CACCCAGGCAAGCCGCCCAAACTCATGATTTATGAGGCGAGTAAGCGGCCCTCAGGGGTC 104
Qy 181 TCCTGCACCTGGAAACAGCGATGAGCTTGGTGGTTTAACTATGTCCTCTGGTACCAACAC 240
Db 103 TCCTGCACCTGGAAACAGCGATGAGCTTGGTGGTTTAACTATGTCCTCTGGTACCAACAG 44
Qy 241 CAGGCTGAGGACGAGCTGATTTACTGTTGTTTATATACA 282
Db 43 CAGGCTGAGGACGAGCTGATTTACTGCTCTCATATGCA 2

RESULT 6
US-10-091-300-28
/ Sequence 28, Application US/10091300
/ Publication No. US20030108545A1
/ GENERAL INFORMATION:
/ APPLICANT: Rockwell, Patricia
/ APPLICANT: Goldstein, Neil I.
/ TITLE OF INVENTION: Combination Methods of Inhibiting Tumor Growth With a Vascular
/ TITLE OF INVENTION: Endothelial Growth Factor Receptor Antagonist
/ FILE REFERENCE: 11245/46211
/ CURRENT APPLICATION NUMBER: US/10/091,300
/ CURRENT FILING DATE: 2002-03-04
/ NUMBER OF SEQ ID NOS: 85
/ SOFTWARE: WordPerfect 8.0 for Windows
/ SEQ ID NO 28
/ LENGTH: 330
/ TYPE: DNA
/ ORGANISM: Human
US-10-091-300-28

Query Match      73.2%; Score 243.6; DB 15; Length 330;
Best Local Similarity 83.6%; Pred. No. 5.1e-73;
Matches 276; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

Qy 1 CAGTCTGCCCGGACTCAGCTCCCTCTGTCGTCGGGTCTCTCTGGACAGTCGGTCAACATC 60
Db 1 CAGTCTGCCCGGACTCAGCTCCCTCTGTCGTCGGGTCTCTCTGGACAGTCGGTCAACATC 60
Qy 61 TCCTGCACCTGGAAACAGCGATGAGCTTGGTGGTTTAACTATGTCCTCTGGTACCAACAC 120
Db 61 TCCTGCACCTGGAAACAGCGATGAGCTTGGTGGTTTAACTATGTCCTCTGGTACCAACAG 120
Qy 121 CACCCAGGCAAGCCGCCCAAACTCATGATTTATGAGGCGAGTAAGCGGCCCTCAGGGGTC 180
Db 121 CACCCAGGCAAGCCGCCCAAACTCATGATTTATGAGGCGAGTAAGCGGCCCTCAGGGGTC 180
Qy 181 TCCTGCACCTGGAAACAGCGATGAGCTTGGTGGTTTAACTATGTCCTCTGGTACCAACAC 240
Db 181 TCCTGCACCTGGAAACAGCGATGAGCTTGGTGGTTTAACTATGTCCTCTGGTACCAACAC 240
Qy 241 CAGGCTGAGGACGAGCTGATTTACTGTTGTTTATATACAACAGTACGACTTTGTTA 300
Db 241 CAGGCTGAGGACGAGCTGATTTACTGTTGTTTATATACAACAGTACGACTTTGTTA 300
Qy 301 TTCGGAAGAGGACCGCGTTGACCGTCTTA 330
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; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rn(D) chain R01
US-09-848-798-137

Query Match 72.0%; Score 239.6; DB 10; Length 324;
Best Local Similarity 86.8%; Pred. No. 1.2e-71;
Matches 276; Conservative 0; Mismatches 39; Indels 3; Gaps 1;

Qy 13 ACTGAGCTCCCTCTGTGTCCTGGGTCTCTGTGACAGTCGGTCACCATCTCCTGCACCTGGA 72
Db 10 ACTGAGCTCCCTCTCGCGCTCCGGGTCTCTGTGACAGTCAGTCACCATCTCCTGCACCTGGA 69
Qy 73 ACCAGCGATGAGCTGGTGGTTATTAACATATGTCTCTGTGTACCAACACCAACCCAGGCAAA 132
Db 70 GCCAGCAGTGACGTTGGTGCTTTATAAGCAGCTCTCTGGTACCAACAACACCCAGGCAAA 129
Qy 133 GCCCCAACTCATGATTATCATGTCTGTATGCGGTCTCAGGGCTCTGATCGCTTC 192
Db 130 GCCCCAAACTCTGACTCATGAGGCACTAAGCGGCCCTCTAGGGGTCTCTGATCGCTTC 188
Qy 193 TCTGGCTCCAACTCTGGCAACACGGCTCCCTGACCATCTCTGGGTCCAGGCTGAGGAC 252
Db 190 TCTGGCTCCAACTCTGGCAACACGGCTCCCTGACCGTCTCTGGGTCTCAGGCTGAGGAT 249
Qy 253 GAGCGTATTTAGTGTGTTTCATATACACCGATAGCACATTTGTTATTCGGAAGAGGG 312
Db 250 GAGCGTGATTTACTGCACTCATTTGCA---GGTAATTCGTGTATATTCGCGGAGGG 306
Qy 313 ACCCGGTTGACCGTCTTA 330
Db 307 ACCAAGCTGACCGTCTTA 324

RESULT 9
US-09-879-813-85
; Sequence 85, Application US/09879813
; Patent No. US20020155453A1
; GENERAL INFORMATION:
; APPLICANT: Neuberger, Michael S.
; APPLICANT: Cumbers, Sarah J.
; TITLE OP INVENTION: Method of Generating Diversity
; FILE REFERENCE: 18396/2005
; CURRENT APPLICATION NUMBER: US/09/879,813
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: 09/828,717
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/GB99/03358
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 85
; LENGTH: 300
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-879-813-85

Query Match 71.8%; Score 239.2; DB 9; Length 300;
Best Local Similarity 89.7%; Pred. No. 1.6e-71;
Matches 269; Conservative 0; Mismatches 28; Indels 3; Gaps 1;

Qy 19 CCTCCTCTGTGTCGGGTCTCTGGACAGTCGGTCACCATCTCCTGCACCTGGAACACG 78
Db 1 CCTGCTCGTGTCGGGTCTCTGGACAGTCGATCACCATCTCTCTGCACCTGGAACACG 60
Qy 79 GATGAGCTGGGTGTATATCATCTCTCTGGTACCAACACCCAGGCAAGCCCC 138
Db 61 AGTGAGCTGGGTGTATATCATCTCTCTGGTACCAACAAACCCAGGCAAGCCCC 120
Qy 139 AAATCATGATTTATGATGTCGCTAAGCGGGCTCTCAGGGGTCTCTGATCGTTCTCTGC 198
Db 121 AAATCATGATTTATGATGTCGCTAAGCGGGCTCTCAGGGGTCTCTGATCGTTCTCTGC 180

```

QY 199 TCCAGTCTGGCAACAGCGCTCCCTGACCATCTCTGGGCTCCAGGCTGAGCAAGAGCT 258
DB 181 TCCAGTCTGGCAACAGCGCTCCCTGACCATCTCTGGGCTCCAGGCTGAGCAAGAGCT 240
QY 259 GATTATTACTGTGTTCATATACCAACAGTACCA---CTTTGTTATTTCGAGAGAGGAC 315
DB 241 GATTATTACTGTGTTCATATACCAACAGTACCA---CTTTGTTATTTCGAGAGAGGAC 300

RESULT 10

US-10-146-505-85
; Sequence 85, Application US/10146505
; Publication No. US20030108889A1
; GENERAL INFORMATION:
; APPLICANT: Sale, Julian E.
; APPLICANT: Neuberger, Michael S.
; APPLICANT: Cumbers, Sarah J.
; TITLE OF INVENTION: Method of Generating Diversity
; FILE REFERENCE: 18396/2005B
; CURRENT APPLICATION NUMBER: US/10/146,505
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/828,717
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 09/879,813
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: PCT/GB99/03358
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: GB 9822104.7
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: GB 9901141.3
; PRIOR FILING DATE: 1998-01-19
; PRIOR APPLICATION NUMBER: GB 9913435.5
; PRIOR FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 85
; LENGTH: 300
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-146-505-85

Query Match 71.8%; Score 239.2; DB 15; Length 300;
Best Local Similarity 89.7%; Pred No. 1.6e-71;
Matches 269; Conservative 0; Mismatches 28; Indels 3; Gaps 1;

QY 199 CTCCCTCTGTGTCTGGGCTCTCTGGACAGTCGGTCAACATCTCTCTGCACTGGAAACGAGC 78
DB 1 CCTGCCTCGTGTCTGGGCTCTCTGGACAGTCGATCACCATCTCTCTGCACTGGAAACGAGC 60
QY 79 GATGACGTGGTGGTATATACATCTCTCTGTACCAACACCCAGGCAAGAGGAGGAGG 138
DB 61 AGTGACGTGGTGGTATATACATCTCTCTGTACCAACACCCAGGCAAGAGGAGGAGG 120
QY 139 AAACATCATGATTATGATGTCGCTAAGCGGGCTCAGGGGCTCTCTGATCGCTTCTCTGGC 198
DB 121 AAACATCATGATTATGATGTCAGTAATCGGCCCTCAGGGATTTCTAATCGCTTCTCTGGC 180
QY 199 TCCAGTCTGGCAACAGCGCTCCCTGACCATCTCTGGGCTCCAGGCTGAGCAAGAGGCT 258
DB 181 TCCAGTCTGGCAACAGCGCTCCCTGACCATCTCTGGGCTCCAGGCTGAGCAAGAGGCT 240
QY 259 GATTATTACTGTGTTCATATACCAACAGTACCA---CTTTGTTATTTCGAGAGAGGAGC 315
DB 241 GATTATTACTGTGTTCATATACCAACAGTACCA---CTTTGTTATTTCGAGAGAGGAGC 300

RESULT 11

US-09-864-761-22661
; Sequence 22661, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.

; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wenheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 22661
; LENGTH: 294
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC02308.1
; OTHER INFORMATION: EXPRESSED IN LONG, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
; OTHER INFORMATION: NT HIT: X14616.1, EVALUATE 0.00e+00
; OTHER INFORMATION: EST HUMAN HIT: A406348.1, EVALUATE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: P01705, EVALUATE 4.00e-45
US-09-864-761-22661
Query Match 71.2%; Score 237; DB 9; Length 294;
Best Local Similarity 91.0%; Pred No. 8.9e-71;
Matches 252; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 20 CTCCCTCTGTGTCTGGGCTCTCTGGACAGTCGGTCAACATCTCTGCACTGGAAACGAGC 79
DB 1 CTGCCTCGTGTCTGGGCTCTCTGGACAGTCGATCACCATCTCTGCACTGGAAACGAGC 60
QY 80 ATGACGTGGTGGTATATACATCTCTCTGGTACCAACACCCAGGCAAGAGGAGGAGC 139

Db 61 GTGATGTTGGAGTTATACCTTGTCTCTGGTACCAACAGCACCAGGCAAGGCCCCCA 120
Qy 140 AACTCATGATTATGATGCTCGCTAAGCGGGCTCAGGGTCTCTGATCGGCTCTCTGGCT 199
Db 121 AACTCATGATTATGAGGCGAGTAAAGCGCCCTCAGGGGTTTCTAATCGCTTCTCTGGCT 180
Qy 200 CCAAGTCTGGCAACACAGCGCTCTCTGACCACTCTCTGGGCTCCAGGCTGAGGACAGGCTG 259
Db 181 CCAAGTCTGGCAACACAGCGCTCTCTGACCACTCTCTGGGCTCCAGGCTGAGGACAGGCTG 240
Qy 260 ATTATGATGTTGTTCTATATACACACAGGCTGAGGCTTT 296
Db 241 ATTATGATGTTGTTCTATATGAGGCTGAGGCTTT 277

RESULT 12

US-10-029-386-15224/c
; Sequence 15224, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: AEMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 15224
; LENGTH: 278
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR22_117.0
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.9
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.4
; OTHER INFORMATION: SWISSPROT HIT: P01709, EVALU0 1.00e-30
; OTHER INFORMATION: NT HIT: X57825.1, EVALU0 0.00e+00
; OTHER INFORMATION: EST_HUMAN HIT: BG759257.1, EVALU0 5.00e-99
US-10-029-386-15224

Query Match 65.9%; Score 219.6; DB 15; Length 278;
Best Local Similarity 89.1%; Pred. No. 8.1e-65;
Matches 237; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 1 CAGTCTCCCGACTCAGCTCCCTCTGCTGCTGGTCTCTCGACAGTGGTCAACATC 60
Db 267 CAGTCTCCCTGATTAGCTCCCTCTGCTGCTGGTCTCTCGACAGTCACTCAACATC 208
Qy 61 TCCTGCACTGGACACAGGATGAGTGGTGGTTAATATCTCTCTGTTACCAACAC 120
Db 207 TCCTGCACTGGACACAGGATGAGTGGTGGTTAATATCTCTCTGTTACCAACAG 148
Qy 121 CACCCAGGCAAGCCCAACCACTCATGATTATGATGCTCGCTAAGCGGGCTCAGGGGTC 180
Db 147 CACCCAGGCAAGCTCCCAACCACTCATGATTATGATGCTCGCTAAGCGGGCTCAGGGGTC 88
Qy 181 TCCTGATGCTCTCTGCTGCTGAGTCTGAGTCTGCAACAGGCTCCCTGACCATCTCTGGGTC 240
Db 87 CCGTATGCTTCTCTGCTGCTGAGTCTGAGTCTGCAACAGGCTCCCTGACCATCTCTGGGTC 28
Qy 241 CAGGCTGAGGACGAGGCTGATTATTA 266
Db 27 CAGGCTGAGGACGAGGCTGATTATTA 2

RESULT 13

Qy 53 TCACCATCTCTGCACTGGACACAGGATGAGTGGTGGTTATTAATATGATGCTCTCTGGT 112

US-09-734-613-15
; Sequence 15, Application US/09734613
; Publication No. US20020088016A1
; GENERAL INFORMATION:
; APPLICANT: BRUGEMANN, Marianne
; TITLE OF INVENTION: MURINE EXPRESSION OF A HUMAN IGA LAMBDA LOCUS
; FILE REFERENCE: 37945-0009
; CURRENT APPLICATION NUMBER: US/09/734,613
; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: PCT/GB99/03632
; PRIOR FILING DATE: 1999-11-03
; PRIOR APPLICATION NUMBER: GB 9823930.4
; PRIOR FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 246
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-734-613-15

Query Match 65.6%; Score 218.4; DB 13; Length 246;
Best Local Similarity 93.4%; Pred. No. 2e-64;
Matches 228; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy 53 TCACCATCTCTGCACTGGACACAGGATGAGTGGTGGTTATTAATATGATGCTCTCTGGT 112
Db 2 TCACCATCTCTGCACTGGACACAGGATGAGTGGTGGTTATTAATATGATGCTCTCTGGT 61
Qy 113 ACCAACACACCCAGGCAAGGCCCCAACTCATGATTATGATGCTGCTAAGCGGGCT 172
Db 62 ACCAACACACCCAGGCAAGGCCCCAACTCATGATTATGAGGTGAGTAATCGGCCCT 121
Qy 173 CAGGGGTCTCTGATGCTCTGCTCTGCTCCAGTCTGGCAACACAGGCTCCCTGACCATCT 232
Db 122 CAGGGGTCTCTGATGCTCTGCTCTGCTCCAGTCTGGCAACACAGGCTCCCTGACCATCT 181
Qy 233 CTGGGCTCCAGGCTCAGGACGAGGCTGATTATTAATGTTGTTTCATATACACAGTAGCA 292
Db 182 CTGGGCTCCAGGCTCAGGACGAGGCTGATTATTAATGTTGTTTCATATACACAGTAGCA 241
Qy 293 CTTT 296
Db 242 CTCT 245

RESULT 14

US-09-734-613-16
; Sequence 16, Application US/09734613
; Publication No. US20020088016A1
; GENERAL INFORMATION:
; APPLICANT: BRUGEMANN, Marianne
; TITLE OF INVENTION: MURINE EXPRESSION OF A HUMAN IGA LAMBDA LOCUS
; FILE REFERENCE: 37945-0009
; CURRENT APPLICATION NUMBER: US/09/734,613
; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: PCT/GB99/03632
; PRIOR FILING DATE: 1999-11-03
; PRIOR APPLICATION NUMBER: GB 9823930.4
; PRIOR FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 243
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-734-613-16

Query Match 64.5%; Score 214.8; DB 13; Length 243;
Best Local Similarity 93.0%; Pred. No. 3.4e-63;
Matches 225; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Db	2	TCACCATCTCTGCACTGGACAGTGGTGGTCTTAACCTTGTCTCTCTGGT	61
Qy	113	ACCAACACACCCAGGCAAGCCCAACTCATGATTTATGATCGCTAAGCGGGCT	172
Db	62	ACCAACACACCCAGGCAAGCCCAACTCATGATTTATGATCGCTAAGCGGGCT	121
Qy	173	CAGGGGTCTCTGATCGCTTCTCTGGCTCCAACTCTGGCAACACGCGCTCCCTGACCATCT	232
Db	122	CAGGGGTCTCTGATCGCTTCTCTGGCTCCAACTCTGGCAACACGCGCTCCCTGACCATCT	181
Qy	233	CTGGGCTCAGGCTGAGGACGAGGCTGATTTACTGTTTATATACAAACAGGAGCA	292
Db	182	CTGGGCTCAGGCTGAGGACGAGGCTGATTTACTGTTTATATACAAACAGGAGCA	241
Qy	293	CT 294	
Db	242	CT 243	

RESULT 15

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US-09-734-613-21
; Sequence 21, Application US/09734613
; Publication No. US2002008016A1
; GENERAL INFORMATION:
; APPLICANT: BRUGSEMAN, Marianne
; TITLE OF INVENTION: MURINE EXPRESSION OF A HUMAN IGA LAMBDA LOCUS
; FILE REFERENCE: 37945-0009
; CURRENT APPLICATION NUMBER: US/09/734,613
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: PCT/GB99/03632
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: GB 9823930.4
; PRIOR FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 246
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-734-613-21

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Query Match 63.2%; Score 210.4; DB 13; Length 246;
Best Local Similarity 91.4%; Pred. No. 1.1e-61;
Matches 223; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy	53	TCACCATCTCTGCACTGGACAGGATGACGTGGTGGTATATACTATGCTCTCTGGT	112
Db	2	TCACCATCTCTGCACTGGACAGGATGACGTGGTGGTATATACTATGCTCTCTGGT	61
Qy	113	ACCAACACACCCAGGCAAGCCCAACTCATGATTTATGATCGCTAAGCGGGCT	172
Db	62	ACCAACACACCCAGGCAAGCCCAACTCATGATTTATGATCGCTAAGCGGGCT	121
Qy	173	CAGGGGTCTCTGATCGCTTCTCTGGCTCCAACTCTGGCAACACGCGCTCCCTGACCATCT	232
Db	122	CAGGGGTCTCTGATCGCTTCTCTGGCTCCAACTCTGGCAACACGCGCTCCCTGACCATCT	181
Qy	233	CTGGGCTCAGGCTGAGGACGAGGCTGATTTACTGTTTATATACAAACAGGAGCA	292
Db	182	CTGGGCTCAGGCTGAGGACGAGGCTGATTTACTGTTTATATACAAACAGGAGCA	241
Qy	293	CTTT 296	
Db	242	CTTT 245	

Search completed: June 19, 2004, 04:36:35
Job time : 285 secs

OM nucleic - nucleic search, using sw model

Run on: June 19, 2004, 03:12:07 ; Search time 1733 Seconds
(without alignments)
5738.088 Million cell updates/sec

Title: US-09-019-441A-1_COPY_58_390

Perfect score: 333

Sequence: 1 cagctgccccgactcagcc.....ccccggttgacctcctaggt 333

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 10684159

Minimum DB seq length: 0

Maximum DB seq length: 333

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.*

1: em_estba.*

2: em_esthum.*

3: em_estin.*

4: em_estmu.*

5: em_estov.*

6: em_estpl.*

7: em_estro.*

8: em_hct.*

9: gb_estl.*

10: gb_est2.*

11: gb_hct.*

12: gb_est3.*

13: gb_est4.*

14: gb_est5.*

15: em_estfun.*

16: em_estom.*

17: em_gss_hum.*

18: em_gss_irv.*

19: em_gss_pln.*

20: em_gss_vrt.*

21: em_gss_fun.*

22: em_gss_mam.*

23: em_gss_mus.*

24: em_gss_pro.*

25: em_gss_rod.*

26: em_gss_phg.*

27: em_gss_vrl.*

28: gb_gssl.*

29: gb_gss2.*

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	237.6	71.4	325	14	CD707555 EST24082
2	231.4	69.5	280	13	BU584333 3392316H1
3	224.4	67.4	258	13	BU584280 1045436H1
4	219.8	66.0	248	14	CD705383 EST21910

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

5	217.6	65.3	260	14	T27942	T27942	EST20865 HU
6	215.6	64.7	307	10	BF825613	BF825613	BCO-BN002
7	214.8	64.5	327	14	CD703527	CD703527	EST20054
8	213.8	64.2	296	14	CD698983	CD698983	EST15506
9	213.4	64.1	313	9	AA327392	AA327392	EST15506
10	212	63.7	327	14	CD698921	CD698921	EST15344
11	211.2	63.4	323	10	AW404118	AW404118	UI-HF-BLO
12	211	63.4	243	13	BU584479	BU584479	46333268H1
13	210	63.1	234	13	BU584573	BU584573	5559803H1
14	209.8	63.0	284	13	BU584480	BU584480	4633413H1
15	206.2	61.9	254	10	AW407182	AW407182	UI-HF-BLO
16	206	61.9	318	13	BX283257	BX283257	EX283257
17	205.4	61.7	248	13	BU584608	BU584608	5837950H1
18	205	61.6	282	10	BE706848	BE706848	QV0-HT036
19	203	61.0	320	13	BU584244	BU584244	2814919H1
20	202.2	60.7	328	14	CD695826	CD695826	EST12349
21	201	60.4	237	13	BU584067	BU584067	1451234H1
22	199.4	59.9	251	14	N47367	N47367	YY56d06.r1
23	198.4	59.6	333	12	BP431103	BP431103	BP431103
24	192.2	57.7	244	14	H22217	H22217	Y138h04.r1
25	191.2	57.4	291	13	BU584284	BU584284	3056744H1
26	191.2	57.4	314	9	AA327386	AA327386	EST30712
27	189.8	57.0	325	14	CD700666	CD700666	EST17190
28	189.2	56.8	287	13	BU584265	BU584265	2921049H1
29	188.4	56.6	310	13	BU584281	BU584281	3046928H1
30	188	56.5	313	12	BP430005	BP430005	BP430005
31	185.8	55.8	293	13	BU584332	BU584332	3392264H1
32	183.6	55.1	214	13	BU584098	BU584098	1635030H1
33	183.6	55.1	294	13	BU584145	BU584145	1960565H1
34	183.2	55.0	235	10	AW806367	AW806367	MR4-UM011
35	183	55.0	281	13	BU584254	BU584254	2877568H1
36	180.2	54.1	217	13	BU584110	BU584110	1695353H1
37	179.8	54.0	307	10	AW407310	AW407310	UI-HF-BLO
38	178.8	53.7	309	13	BU584379	BU584379	3814751H1
39	177	53.2	309	12	BP429773	BP429773	BP429773
40	175	52.6	285	13	BU584279	BU584279	3042631H1
41	175	52.6	315	12	BM823400	BM823400	K-BST0094
42	174.4	52.4	331	14	CD692574	CD692574	EST9097.h
43	173.6	52.1	280	13	BU584640	BU584640	6102171H1
44	173	52.0	221	10	AW407470	AW407470	UI-HF-BLO
45	173	52.0	305	12	BP429335	BP429335	BP429335

ALIGNMENTS

RESULT 1	CD707555	325 bp	mRNA	linear	EST 25-JUN-2003
LOCUS	EST24082	human nasopharynx	Homo sapiens	cDNA, mRNA	sequence.
DEFINITION	CD707555				
ACCESSION	CD707555				
VERSION	CD707555.1	GI:32238185			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Bukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and Zeng,Y.-X.				
TITLE	Transcriptional Gene Expression Profile of Human Nasopharynx				
JOURNAL	Unpublished (2003)				
COMMENT	Contact: Yixin Zeng Cancer Center Sun Yat-sen University 651 Dongfeng Road East, Guangzhou 510060, China Tel: 86-1380-9770-743 Fax: 86-20-8775-4506 Email: yxzeng@zsuns.edu.cn.				

Location/Qualifiers

1..325
/organism="Homo sapiens"
/mol_type="mRNA"

FEATURES
source

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/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA
library from southern Chinese"

ORIGIN
Query Match 71.4%; Score 237.6; DB 14; Length 325;
Best Local Similarity 94.6%; Pred. No. 7.7e-57;
Matches 246; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 CAGTCTCCCGACTCAGCCTCCCTGTGTCTGGGTCCTCTGACAGTCGGTCCACATC 60
DB 66 CAGTCTCCCGACTCAGCCTCCCTGTGTCTGGGTCCTCTGACAGTCGGTCCACATC 125
QY 61 TCTGCACTGGAACACGAGTACGTTGGTGTATTAATATGTCCTCTGACAGTCGGTCCACATC 120
DB 126 TCTGCACTGGAACACGAGTACGTTGGTGTATTAATATGTCCTCTGACAGTCGGTCCACATC 185
QY 121 CACCCAGGCAAGCCCAACTCATGATTTATGATGTCGTAAGCGGGCTCAGGGTC 180
DB 186 GACCCAGGCAAGCCCAACTCATGATTTATGATGTCGTAAGCGGGCTCAGGGTC 245
QY 181 TCTGATCGCTTCTGCTGCTCCAGTCTGCAACAGCGCTCCCTGACCATCTCTGGGCTC 240
DB 246 TCTAATGCTTCTGCTGCTCCAGTCTGCAACAGCGCTCCCTGACCATCTCTGGGCTC 305
QY 241 CAGGCTGAGGACGAGGCTGA 260
DB 306 CAGGCTGAGGACGAGGCTGA 325

RESULT 2
BU584333 280 bp mRNA linear EST 20-SEP-2002
LOCUS 3392316H1 LUNGNOT28 Homo sapiens cDNA clone 3392316 5', mRNA
DEFINITION
sequence.
ACCESSION BU584333
VERSION BU584333.1 GI:23258298
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 280)
AUTHORS Collins,J.E., Goward,M.E., Cole,C.G., Smink,I.J., Huckle,E.J.,
Knowles,S., Bye,J.M., Beare,D.M. and Dunham,I.
TITLE Re-evaluating Human Gene Annotation: A Second Generation Analysis
of Chromosome 22
JOURNAL Unpublished (2002)
COMMENT Contact: Panzer SR
Incyte Genomics, Inc.
3160 Porter Drive, Palo Alto, CA 94304, USA
Tel: 650 845 4682
Fax: 650 845 5495
Email: spanzer@incyte.com.
Location/Qualifiers
1..280
/organism="Homo sapiens"
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/clone="3392316"
/tissue_type="lung"
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ORIGIN
Query Match 69.4%; Score 224.4; DB 13; Length 258;
Best Local Similarity 91.9%; Pred. No. 3.9e-53;
Matches 237; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 30 GTCTGGGTCTCTCTGACAGTCGGTCCACATCTCTGCACTGGAACACGAGTCAGTTGG 89
DB 1 GTCCGGGTCTCTCTGACAGTCAGTCACCATCTCTCTGCACTGGAACACGAGTCAGTTGG 60
QY 90 TGGTTATAACTATGTCCTCTGTTACCAACACCCAGGCAAGCCCAAACTCATGAT 149
DB 61 TCGTTATAAATATGTCCTCTGTTACCAACACCCAGGCAAGCCCAAACTCATGAT 120
QY 150 TTATGATGTCGCTAAGCGGGCTCAGGGGTCTCTGATGCTTCTCTGGCTCCAACTCTGG 209
DB 121 TTATGAGGTGAGTAAAGCGGGCTCAGGGGTCTCTGATGCTTCTCTGGCTCCAACTCTGG 180
QY 210 CAACACGGCTCTCTGACCATCTCTGGGCTCCAGGCTCAGAGCAGGCTGATTAATCTG 269
DB 181 CAACACGGCTCTCTGACCATCTCTGGGCTCCAGGCTCAGAGCAGGCTGATTAATCTG 240
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QY 270 TTGTTTCATATACACACG 287
Db 241 CTGCTCATTTACAGCAG 258

RESULT 4
CD705383 248 bp mRNA linear EST 25-JUN-2003
LOCUS EST21910 human nasopharynx Homo sapiens cDNA, mRNA sequence.
DEFINITION CD705383
ACCESSION CD705383
VERSION CD705383.1 GI:32236013
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 248)
AUTHORS Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and
Zeng, Y.-X.
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: Vixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gzsums.edu.cn.

FEATURES
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1..248
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/tissue="nasopharynx"
/clone_lib="human nasopharynx"
/notes="ESTs generated from a normal nasopharynx cDNA
library from southern Chinese"

ORIGIN
source
Query Match 66.0%; Score 219.8; DB 14; Length 248;
Best Local Similarity 93.1%; Pred. No. 7.8e-52;
Matches 230; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1 CAGTCTGCCCGACGACGCTCCCTCTGCTGGTCTCTGACAGTGGTACACCATC 60
Db 2 CAGTCTGCCCGACGACGCTCCCTCTGCTGGTCTCTGACAGTGGTACACCATC 61

QY 61 TCCTGCACTGGAACAGCAGATGAGTGGTGGTTATTAATATGCTCTCTGTTACCAAC 120
Db 62 TCCTGCACTGGAACAGCAGATGAGTGGTGGTTATTAATATGCTCTCTGTTACCAAC 121

QY 121 CACCAGCAAGCCCCCAATCATGATTTATGATGCTAGCGGTAGCGGGCTCAGGGTTC 180
Db 122 CACCAGCAAGCAACCAATCATGATTTATGCTGCTAGCGGTAGCGGGCTCAGGGTTC 181

QY 181 TCTGATCCCTTCTCTGGCTCCCAAGTCTGGCAACAGCGGCTCCCTGACCATCTCTGGGCTC 240
Db 182 TCTAATCCCTTCTCTGGCTCCCAAGTCTGGCAACAGCGGCTCCCTGACCATCTCTGGGCTC 241

QY 241 CAGGCTG 247
Db 242 CAGGCTG 248

RESULT 5
T27942 260 bp mRNA linear EST 06-SEP-1995
LOCUS EST20865 Human Spleen Homo sapiens cDNA 5' end similar to
DEFINITION immunoglobulin lambda light chain V.J.C regions (GB:L03633)
(HT:3223), mRNA sequence.
ACCESSION T27942
VERSION T27942.1 GI:610040

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EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 260)
AUTHORS Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W.,
Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
FitzGerald, L.M., Fritchman, J.L., Geoghagen, N.S.M.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkley, P.S.,
Kelley, J.M., Kline, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M.,
Merrick, J.M., Moreno-Palacios, R.F., McDonald, L.A., Nguyen, D.T.,
Pellegri, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L.,
Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R.,
Weidman, J.F., Li, Y., Bednarek, D.P., Cao, L., Cepeda, M.A.,
Coleman, T.A., Collins, E.-J., Dimke, D., Feng, P., Ferrie, A.,
Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M.,
Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., J.H., Li, H.,
Meisner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C.,
Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A.,
Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.
TITLE Initial Assessment of Human Gene Diversity and Expression Patterns
Based Upon 83 Million Basepairs of cDNA Sequence
JOURNAL Nature 377, 3-174 (1995)
MEDLINE 96026280
PUBMED 7566098
COMMENT Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@tdb.tigr.org
For clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
(tdbinfo@tdb.tigr.org)
Seq primer: M13 Reverse.
FEATURES
source
1..260
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="ATCC (inhost):100584"
/db_xref="taxon:9606"
/clone_lib="Human Spleen"
/notes="Organ: spleen"

ORIGIN
source
Query Match 65.3%; Score 217.6; DB 14; Length 260;
Best Local Similarity 89.6%; Pred. No. 3.4e-51;
Matches 232; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 34 GGCTCTCCCTGGACAGTGGTACCATCTCTGACACGAGCAACAGCGATGACGTTGGTGT 93
Db 2 GGCTCTCCCTGGACAGTGGTACCATCTCTGACACGAGCAACAGCGATGACGTTGGTGT 61

QY 94 TATAAATATGTTCTCTGGTACCAACACCAAGGCAAGGCCCCCAAACTCATGATTAT 153
Db 62 TATAAATATGTTCTCTGGTACCAACACCAAGGCAAGGCCCCCAAACTCATGATTAT 121

QY 154 GATGTCGCTAAGCGGCTCAGGGCTCTGATGCTGCTCTCTGCTCCCAAGTCTGGCAAC 213
Db 122 GAGTCAGTAAATCGGGCTCAGGGCTCAGGGCTCAGGGCTCAGGGCTCAGGGCTCAG 181

QY 214 ACGGCTCTCCCTGACCATCTCTGGGCTCCAGGCTGAGGACGAGGCTGATTATTTACTGTGT 273
Db 182 ACGGCTCTCCCTGACCATCTCTGGGCTCCAGGCTGAGGACGAGGCTGATTATTTACTGTGT 241

QY 274 TCATATACACACAGTAGCA 292
Db 242 TCATATACACACAGTAGCA 260

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CD698983
EST.
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 296)
Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-X., Pan,Z.-G. and Zeng,Y.-X.
Transcriptional Gene Expression Profile of Human Nasopharynx Unpublished (2003)
Contact: YiXin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gzsums.edu.cn.

FEATURES
source
1..296
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/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/notes="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

ORIGIN
Query Match 64.2%; Score 213.8; DB 14; Length 296;
Best Local Similarity 89.5%; Pred.No. 4.4e-50;
Matches 230; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 1 CAGTCTGCCCGACTCAGCCCTCTGTCTCTGGTTCTCTGCACAGTCGGTCAACCATC 60
| | | | |
Db 40 CAGTCTGCCCTGACTCAGCTTGCTCGTCTGGTCTCTGCACAGTCGGTCAACCATC 99
| | | | |

QY 61 TCCTGCACCTGGAAACACAGCGATGACGTTGGTGGTTATAACTATGTCCTCGTACCAACAC 120
| | | | |
Db 100 TCCTGCACCTGGAAACACAGCGATGTTGGAGTCTATGCTTGGTCTCTGGTACCAACA 159
| | | | |

QY 121 CACCAGGCGAAGCCCCAACCTCATGATTATGATGCGCTAAGCGGGCTCGAGGGCTC 180
| | | | |
Db 160 CACCCAGGCGAAGCCCCAACCTCATCATTTATAAGGGCTATTAACCGGGCTCGAGGGCTT 219
| | | | |

QY 181 TGTGATCGCTTCTCTGCTCTCAAAGTCGGCAACACAGCGCTCCCTCGACATCTCTGGGCTC 240
| | | | |
Db 220 TCTATGCTTCTCTGCTCTCAAAGTCGGCAACACAGCGCTCCCTCGACATCTCTGGGCTC 279
| | | | |

QY 241 CAGCTTGAGCACGAGGC 257
| | | | |
Db 280 CAGCTTGAGCACGAGGC 296
| | | | |

RESULT 9
AA327392
LOCUS
DEFINITION
EST30721 Colon I Homo sapiens cDNA 5' end similar to similar to
immunoglobulin lambda chain, mRNA sequence.
AA327392
AA327392.1 GI:1979637
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 313)
Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.G., Lee,N.H., Kirkness,E.F., Weinscock,K.G., Gockayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,

CD698821
 CD698821.1 GI:32227508
 EST.
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 327)
 Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and Zeng, Y.-X.
 Transcriptional Gene Expression Profile of Human Nasopharynx
 Unpublished (2003)
 JOURNAL
 COMMENT
 Contact: Yixin Zeng
 Cancer Center
 Sun Yat-sen University
 651 Dongfeng Road East, Guangzhou 510060, China
 Tel: 86-1380-9770-743
 Fax: 86-20-8775-4506
 Email: yxzeng@gzsums.edu.cn.

FEATURES
 source
 1..327
 Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3057727"
 /tissue_type="lymph"
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 /cell_line="MGC85"
 /lab_host="DH10B (UT1)"
 /clone_lib="NIH MGC 37"
 /note="Vector: p7713-Pac; Site_1: NotI; Site_2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (1.5-2.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaudo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN
 Query Match 63.7%; Score 212; DB 14; Length 327;
 Best Local Similarity 88.5%; Pred. No. 1.5e-49;
 Matches 230; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
 QY 1 CAGTCTGCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCTCGACAGTCGGTCAACATC 60
 Db 68 CAGTCTGCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCTCGACAGTCGGTCAACATC 127
 QY 61 TCCTGCACTGAACCGGAGTGGTGGTATTAATGCTCTCTGTGACCAAC 120
 Db 128 TCATGCACTGAACCGGAGTGGTGGTATTAATGCTCTCTGTGACCAAC 187
 QY 121 CACCAGCAAGCCCAACTCATGATTTATGATTCGTAATGCGGCGCTCAGGGGTC 180
 Db 188 CACCAGCAAGCCCAACTCATGATTTATGATTCGTAATGCGGCGCTCAGGGGTC 247
 QY 181 TCTGATCGTCTCTGGTCCAGTCTGGCAACAGCGCTCCCTGACCATCTCTGGGCTC 240
 Db 248 TCTAATCGTCTCTGGTCCAGTCTGGCAACAGCGCTCCCTGACCATCTCTGGGCTC 307
 QY 241 CAGGCTGAGGACGAGGCTGA 260
 Db 308 CCGCTGAGGACGAGGCTGA 327

RESULT 11
 AM404118
 LOCUS
 DEFINITION
 UI-EF-BLO-abu-b-04-0-UI.r1 NIH MGC 37 Homo sapiens cDNA clone
 IMAGE:3057727 5', mRNA sequence.
 ACCESSION
 AM404118
 VERSION
 AM404118.1 GI:6923175
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 323)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 JOURNAL
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov

Eco RI site shown at the beginning of the sequence.
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: M.B. Soares Lab
 cDNA Library Arrayed by: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/MLNL at: www.bio.lnl.gov/bbrp/image/image.html
 Seq primer: M13 Forward.

FEATURES
 Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3057727"
 /tissue_type="lymph"
 /cell_type="germinal center B cells"
 /cell_line="MGC85"
 /lab_host="DH10B (UT1)"
 /clone_lib="NIH MGC 37"
 /note="Vector: p7713-Pac; Site_1: NotI; Site_2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (1.5-2.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaudo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN
 Query Match 63.4%; Score 211.2; DB 10; Length 323;
 Best Local Similarity 86.2%; Pred. No. 2.6e-49;
 Matches 250; Conservative 0; Mismatches 28; Indels 12; Gaps 1;
 QY 1 CAGTCTGCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCTCGACAGTCGGTCAACATC 60
 Db 39 CAGTCTGCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCTCGACAGTCGGTCAACATC 98
 QY 61 TCTGATCGTCTCTGGTCCAGTCTGGCAACAGCGCTCCCTGACCATCTCTGGGCTC 120
 Db 99 TCTGATCGTCTCTGGTCCAGTCTGGCAACAGCGCTCCCTGACCATCTCTGGGCTC 146
 QY 121 CACCAGCAAGCCCAACTCATGATTTATGATTCGTAATGCGGCGCTCAGGGGTC 180
 Db 147 CACCAGCAAGCCCAACTCATGATTTATGATTCGTAATGCGGCGCTCAGGGGTC 206
 QY 181 TCTGATCGTCTCTGGTCCAGTCTGGCAACAGCGCTCCCTGACCATCTCTGGGCTC 240
 Db 207 TCTAATCGTCTCTGGTCCAGTCTGGCAACAGCGCTCCCTGACCATCTCTGGGCTC 266
 QY 241 CAGGCTGAGGACGAGGCTGATTTACTGTTGTTATATACCAACAGTAG 290
 Db 267 CAGGCTGAGGACGAGGCTGATTTACTGTTGTTATATACCAACAGTAG 316

RESULT 12
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 LOCUS
 DEFINITION
 BU584479 GELADIT02 Homo sapiens cDNA clone 4633268 5', mRNA sequence.
 ACCESSION
 BU584479
 VERSION
 BU584479.1 GI:23258444
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 243)
 Collins, J.E., Goward, M.E., Cole, C.G., Smink, L.J., Huckle, E.J., Knowles, S., Bye, J.M., Beare, D.M. and Dunham, I.
 Re-evaluating Human Gene Annotation: A Second Generation Analysis of Chromosome 22
 Unpublished (2002)
 JOURNAL
 COMMENT
 Contact: Panzer SR
 Incyte Genomics, Inc.
 3160 Porter Drive, Palo Alto, CA 94304, USA

CD698821
 CD698821.1 GI:32227508
 EST.
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 327)
 Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and Zeng, Y.-X.
 Transcriptional Gene Expression Profile of Human Nasopharynx
 Unpublished (2003)
 JOURNAL
 COMMENT
 Contact: Yixin Zeng
 Cancer Center
 Sun Yat-sen University
 651 Dongfeng Road East, Guangzhou 510060, China
 Tel: 86-1380-9770-743
 Fax: 86-20-8775-4506
 Email: yxzeng@gzsums.edu.cn.

FEATURES
 source
 1..327
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
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 /tissue_type="normal nasopharynx"
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ORIGIN
 Query Match 63.7%; Score 212; DB 14; Length 327;
 Best Local Similarity 88.5%; Pred. No. 1.5e-49;
 Matches 230; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
 QY 1 CAGTCTGCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCTCGACAGTCGGTCAACATC 60
 Db 68 CAGTCTGCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCTCGACAGTCGGTCAACATC 127
 QY 61 TCCTGCACTGAACCGGAGTGGTGGTATTAATGCTCTCTGTGACCAAC 120
 Db 128 TCATGCACTGAACCGGAGTGGTGGTATTAATGCTCTCTGTGACCAAC 187
 QY 121 CACCAGCAAGCCCAACTCATGATTTATGATTCGTAATGCGGCGCTCAGGGGTC 180
 Db 188 CACCAGCAAGCCCAACTCATGATTTATGATTCGTAATGCGGCGCTCAGGGGTC 247
 QY 181 TCTGATCGTCTCTGGTCCAGTCTGGCAACAGCGCTCCCTGACCATCTCTGGGCTC 240
 Db 248 TCTAATCGTCTCTGGTCCAGTCTGGCAACAGCGCTCCCTGACCATCTCTGGGCTC 307
 QY 241 CAGGCTGAGGACGAGGCTGA 260
 Db 308 CCGCTGAGGACGAGGCTGA 327

RESULT 11
 AM404118
 LOCUS
 DEFINITION
 UI-EF-BLO-abu-b-04-0-UI.r1 NIH MGC 37 Homo sapiens cDNA clone
 IMAGE:3057727 5', mRNA sequence.
 ACCESSION
 AM404118
 VERSION
 AM404118.1 GI:6923175
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 323)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 JOURNAL
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov

Tel: 650 845 4682

Fax: 650 845 5495

Email: spanzer@incyte.com.

Location/Qualifiers

FEATURES

source

1..243

/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="4633268"
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/note="gallbladder, cholecystitis, 18F"

ORIGIN

Query Match 63.4%; Score 211; DB 13; Length 243;
Best Local Similarity 91.8%; Pred. No. 2.5e-49;
Matches 223; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 49 TCGGTACCAATCTCTGCACTGGAAACCGAGATGAGTGGTGGTATTAACATATGCTCC 108

DB 1 TCGATCACCATCTCTGCACTGGAAACCGAGATGAGTGGTGGTATTAACATATGCTCC 60

QY 109 TGGTACCAACACCCAGGCAAGCCCAACTCATGATTTATGATGCTGCTAAGCGG 168

DB 61 TGGTACCAACACCCAGGCAAGCCCAACTCATGATTTATGATGCTGCTAAGCGG 120

QY 169 GCCTCAGGGGCTCTGATGCTTCTCTGGCTCCAAAGTCTGGCAACACGGCTCCCTGACC 228

DB 121 CCCTCAGGGGTTCTAATCGTCTCTGGCTCCAAAGTCTGGCAACACGGCTCCCTGACC 180

QY 229 ATCTCTGGCTCCAGGCTGAGACGAGCTGATTTATGATGCTGCTAAGCGG 288

DB 181 ATCTCTGGCTCCAGGCTGAGACGAGCTGATTTATGATGCTGCTAAGCGG 240

QY 289 AGC 291

DB 241 AGC 243

RESULT 13

BU584573

LOCUS 5559803H1 BRSTDIT01 Homo sapiens cDNA clone 5559803 5', mRNA

DEFINITION 234 bp mRNA linear EST 20-SEP-2002

sequence.

ACCESSION BU584573

VERSION BU584573.1 GI:23258538

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 234)

Knowles, S.; Bye, J.M.; Goward, M.E.; Cole, C.G.; Smink, L.J.; Huckle, E.J.,

Re-evaluating Human Gene Annotation: A Second Generation Analysis

of Chromosome 22

Unpublished (2002)

Contact: Panzer SR

Incyte Genomics, Inc.

3160 Porter Drive, Palo Alto, CA 94304, USA

Tel: 650 845 4682

Fax: 650 845 5495

Email: spanzer@incyte.com.

Location/Qualifiers

1..234

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="5559803"

/tissue_type="breast"

/clone_lib="BRSTDIT01"

/note="breast, PF changes, mw/intraductal cancer, 48F"

ORIGIN

Query Match 63.0%; Score 209.8; DB 13; Length 264;

Best Local Similarity 89.4%; Pred. No. 5.7e-49;

Matches 237; Conservative 0; Mismatches 27; Indels 1; Gaps 1;

QY 50 CGGTACCAATCTCTGCACTGGAAACCGAGATGAGTGGTGGTATTAACATATGCTCC 109

DB 1 CGATCACCATCTCTGCACTGGAAACCGAGATGAGTGGTGGTATTAACATATGCTCC 60

QY 110 GGTACCAACACCCAGGCAAGCCCAACTCATGATTTATGATGCTGCTAAGCGG 169

DB 61 GGTACCAACACCCAGGCAAGCCCAACTCATGATTTATGATGCTGCTAAGCGG 120

QY 170 CCTCAGGGGCTCTGATGCTTCTCTGGCTCCAAAGTCTGGCAACACGGCTCCCTGACC 229

DB 121 CCTCAGGGGTTCTAAT-6CTTCTCTGGCTCCAAAGTCTGGCAACACGGCTCCCTGACC 179

Query Match 63.1%; Score 210; DB 13; Length 234;

Best Local Similarity 93.6%; Pred. No. 4.7e-49;

Matches 219; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 49 TCGGTACCAATCTCTGCACTGGAAACCGAGATGAGTGGTGGTATTAACATATGCTCC 108

DB 1 TCGATCACCATCTCTGCACTGGAAACCGAGATGAGTGGTGGTATTAACATATGCTCC 60

QY 109 TGGTACCAACACCCAGGCAAGCCCAACTCATGATTTATGATGCTGCTAAGCGG 168

DB 61 TGGTACCAACACCCAGGCAAGCCCAACTCATGATTTATGATGCTGCTAAGCGG 120

QY 169 GCCTCAGGGGCTCTGATGCTTCTCTGGCTCCAAAGTCTGGCAACACGGCTCCCTGACC 228

DB 121 CCCTCAGGGGTTCTAATCGTCTCTGGCTCCAAAGTCTGGCAACACGGCTCCCTGACC 180

QY 229 ATCTCTGGCTCCAGGCTGAGACGAGCTGATTTATGATGCTGCTAAGCGG 282

DB 181 ATCTCTGGCTCCAGGCTGAGACGAGCTGATTTATGATGCTGCTAAGCGG 234

RESULT 14

BU584480

LOCUS 4633413H1 GBLADIT02 Homo sapiens cDNA clone 4633413 5', mRNA

DEFINITION 264 bp mRNA linear EST 20-SEP-2002

sequence.

ACCESSION BU584480

VERSION BU584480.1 GI:23258445

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 264)

Knowles, S.; Bye, J.M.; Goward, M.E.; Cole, C.G.; Smink, L.J.; Huckle, E.J.,

Re-evaluating Human Gene Annotation: A Second Generation Analysis

of Chromosome 22

Unpublished (2002)

Contact: Panzer SR

Incyte Genomics, Inc.

3160 Porter Drive, Palo Alto, CA 94304, USA

Tel: 650 845 4682

Fax: 650 845 5495

Email: spanzer@incyte.com.

Location/Qualifiers

1..264

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="4633413"

/tissue_type="gallbladder"

/clone_lib="GBLADIT02"

/note="gallbladder, cholecystitis, 18F"

ORIGIN

Query Match 63.0%; Score 209.8; DB 13; Length 264;

Best Local Similarity 89.4%; Pred. No. 5.7e-49;

Matches 237; Conservative 0; Mismatches 27; Indels 1; Gaps 1;

QY 50 CGGTACCAATCTCTGCACTGGAAACCGAGATGAGTGGTGGTATTAACATATGCTCC 109

DB 1 CGATCACCATCTCTGCACTGGAAACCGAGATGAGTGGTGGTATTAACATATGCTCC 60

QY 110 GGTACCAACACCCAGGCAAGCCCAACTCATGATTTATGATGCTGCTAAGCGG 169

DB 61 GGTACCAACACCCAGGCAAGCCCAACTCATGATTTATGATGCTGCTAAGCGG 120

QY 170 CCTCAGGGGCTCTGATGCTTCTCTGGCTCCAAAGTCTGGCAACACGGCTCCCTGACC 229

DB 121 CCTCAGGGGTTCTAAT-6CTTCTCTGGCTCCAAAGTCTGGCAACACGGCTCCCTGACC 179

QY 230 TCTCTGGGCTCCAGGCTGAGGACGAGCTGATTACTTGTGTGTCTATATACACCAAGTA 289
Db 180 TCTCTGGGCTCCAGGCTGAGGACGAGCTGATTACTTGTGTGTCTATATACCAAGTAGTA 239
QY 290 GCACCTTTCTTATTCGGAGAGGGAC 314
Db 240 GCACTCCAGTCTTCGGAACCTGGAC 264

RESULT 15

AW407182 254 bp mRNA linear EST 16-FEB-2000
LOCUS UI-HF-BL0-ade-g-06-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
DEFINITION IMAGE:3061427 5', mRNA sequence.

ACCESSION AM407182
VERSION AM407182.1 GI:6926239
KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 254)

NIH-MGC <http://mgi.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: M.B. Soares Lab

cDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www.bio.llnl.gov/bbrp/image/image.html

Seq primer: M13 Forward.

FEATURES

source

1..254

Location/Qualifiers

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/lab_host="DH10B (LTI)"

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/note="Vector: p773-Pac; Site 1: NotI; Site 2: Eco RI;

Constructed from size fractionated cytoplasmic mRNA

(1.5-2.5kb). Directionally cloned. Cells provided by Louis

M. Staudt, Ph.D. Library preparation by Maria de Fatima

Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Query Match 61.9%; Score 206.2; DB 10; Length 254;

Best Local Similarity 94.3%; Pred. No. 6e-48;

Matches 214; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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Db 28 CAGTGTGCCCTGACTCAGCTGCGCTCCGTGTGGGTCTCTGGACAGTGGTCAACATC 87

QY 61 TCCTGCACTGAACACGAGTGGTGGTGTATTAATATGTTCTCTGGTACCAACAC 120

Db 88 TCCTGCACTGAACACGAGTGGTGGTGTATTAATATGTTCTCTGGTACCAACAA 147

QY 121 CACCCAGCAAGCCGCCCAAACTCATGATTTATGATGTGCTAAGCGGGCTCAGGGGTC 180

Db 148 CACCCAGCAAGCCGCCCAAACTCATGATTTATGATGTGCTAAGCGGGCTCAGGGGTT 207

QY 181 TCTGATCGCTTCTCTGGCTCCAGTCTGGCAACAGGGCTCCCTGAC 227

Db 208 TCTAATCGCTTCTCTGGCTCCAGTCTGGCAACAGGGCTCCCTGAC 254

OM nucleic - nucleic search, using sw model

Run on: June 19, 2004, 05:42:35 ; Search time 1845 Seconds
(without alignments)
8833.052 Million cell updates/sec

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Perfect score: 376
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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 3186280

Minimum DB seq length: 0
Maximum DB seq length: 376

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pri.*
- 10: gb_ro.*
- 11: gb_scs.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
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- 21: em_or.*
- 22: em_ov.*
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- 24: em_ph.*
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- 27: em_sts.*
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- 31: em_htg_inv.*
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- 33: em_htg_mus.*
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- 35: em_htg_rtd.*
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- 37: em_htg_vrt.*
- 38: em_sy.*
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- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	275.6	73.3	373	9	MMU57558	U57558 Macaca mla
2	270	71.8	363	9	MMU57559	U57559 Macaca mla
3	268.4	71.4	363	9	HSU279514	AJ279514 Homo sapi
4	268.4	71.4	363	9	HSU80179	U80179 Human immun
5	263.4	70.1	366	9	HSU279520	AJ279520 Homo sapi
6	263	69.9	368	9	HSU80180	U80180 Human immun
7	260.4	69.3	363	9	HSU245032	AJ245032 Homo sapi
8	257.2	68.4	363	9	HSU279522	AJ279522 Homo sapi
9	255.6	68.0	363	9	HSU244946	AJ244946 Homo sapi
10	255.6	68.0	363	9	HSU279549	AJ279549 Homo sapi
11	255.4	67.9	366	9	HSU80141	U80141 Human immun
12	254.2	67.6	364	9	HSU80125	U80125 Human immun
13	254	67.6	375	9	HSU389176	AJ389176 Homo sapi
14	253	67.3	364	9	AY376082	AY376082 Homo sapi
15	252.4	67.1	363	9	HSU556684	AJ556684 Homo sapi
16	252.2	67.1	366	9	HSU80176	U80176 Human immun
17	251.4	66.9	312	9	HUMIGHCAE	L10093 Human Ig ge
18	250	66.5	354	9	HSU45015	AJ245015 Homo sapi
19	248.4	66.1	354	9	HSU45026	AJ245026 Homo sapi
20	247.8	65.9	308	9	HUMIGHCAD	L10091 Human Ig ge
21	247.6	65.9	360	9	HUMIGHVRN	L12197 Human (Clon
22	247.6	65.9	375	9	HSU45023	AJ245023 Homo sapi
23	247.4	65.8	363	9	HSU45027	AJ245027 Homo sapi
24	246.4	65.5	357	9	U00532	U00532 Human immun
25	246	65.4	360	9	HSU45034	AJ245034 Homo sapi
26	245.8	65.4	366	9	AF455548	AF455548 Homo sapi
27	245.6	65.3	369	9	HSU45060	AJ245060 Homo sapi
28	244.6	65.1	372	6	E12189	E12189 DNA encodin
29	244.6	65.1	375	9	HSNMEMBO	Z46285 H. sapiens r
30	244.4	65.0	360	9	HSU44954	AJ244954 Homo sapi
31	244.2	64.9	366	9	HSU44995	AJ244995 Homo sapi
32	244	64.9	369	9	U00571	U00571 Human immun
33	243.6	64.8	365	9	HSU80142	U80142 Human immun
34	243.2	64.7	354	6	AX355946	AX355946 Sequence
35	243	64.6	372	9	HSU44933	AJ244933 Homo sapi
36	242.8	64.6	371	9	HSU80126	U80126 Human immun
37	242.6	64.5	365	9	HSU279527	AJ279527 Homo sapi
38	242	64.4	317	9	HSU96389	U96389 Homo sapien
39	242	64.4	357	9	AB066903	AB066903 Homo sapi
40	241.8	64.3	363	9	HSU300792	AJ300792 Homo sapi
41	241.4	64.2	296	6	AX470330	AX470330 Sequence
42	241.2	64.1	360	9	HSVH4IC4M	X65736 H. sapiens D
43	241.2	64.1	363	9	HSU44948	AJ244948 Homo sapi
44	240.2	63.9	322	9	HUMIGHCAE	L10092 Human Ig ge
45	240.2	63.9	351	9	AB063656	AB063656 Homo sapi

ALIGNMENTS

RESULT 1	MMU57558	373 bp	mRNA	linear	PRI 02-OCT-1996
LOCUS	Macaca mulatta Ig rearranged heavy chain variable region, anti-RBC				
DEFINITION	antibody, mRNA, partial cds.				
ACCESSION	U57558				
VERSION	U57558.1	GI:1575063			
KEYWORDS					
SOURCE	Macaca mulatta (rhesus monkey)				
ORGANISM	Macaca mulatta				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Rutheria; Primates; Catarrhini; Cercopitheidae;				
	Cercopitheinae; Macaca.				
REFERENCE	1 (bases 1 to 373)				
AUTHORS	Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Blancher, A.				

TITLE	JOURNAL	REFERENCE	AUTHORS
and Capra, J.D. Variable Region Gene Segment Utilization in Rhesus Monkey Hybridomas Producing Human Red Blood Cell-Specific Antibodies: Predominance of the VH4 Family but not VH4-21 (V4-34)	Unpublished	2	(bases 1 to 373) Andris, J.S., Muller, A.B., Abraham, S.R., Cunningham, S., Blancher, A. and Capra, J.D.
			Direct Submission
			Submitted (06-Mar-1996)
			J.S. Andris, Molecular Immunology Center, University of Texas Southwestern Medical Center, 6000 Harry Hines Blvd., Dallas, TX 75235-9140, USA
			Location/Qualifiers
			1. .373
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ORIGIN

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61	CGTGTCCCTCACCTGGCTGT	CTCTGTGTGGCTCTGT	CACAGTAGTAACTGTGTGACCTG	120
64	CGTGTCCCTCACCTGGCTGT	CTCTGTGTAACTCCAT	CACAGTGGTTATGGCTGGAGCTG	123
121	GAATCGCGCAGCCGCCAGGA	AGGAGCTGGAGTGGATTGCA	AGTAATCTCTGTAGTGTGTGG	180
124	GATCGCGCAGCCGCCAGGA	AGGAGCTGGAGTGGATTGGGT	ATATCTGTTTAAATAGTGG	183
181	GGCCACCAACTACAACCC	CGTCCCTCAAGAGTCGAGTCAT	CATTTCACAAGACAAGTCCAA	240
184	TAGCACCGAGTACAACCC	CTCCCTCAAGAGTCGAGTCAC	CATTTCANAAGACAAGTCCAA	243
241	GAACAGATTCTCCGTGAAC	CTCTGTGTACCGCGCGGACA	CGGCCGTGTATTACTG	300
244	GAACAGATTCTCCGTGAAC	CTCTGTGTACCGCGCGGACA	CGGCCGTGTATTACTG	303
301	TGCCAGAGATTGGGCCCAAT	ATAGCTGGAAACAACGCTAG	AGTCTTCTCGGGCCAGGGAGTCC	360
304	TCCGAGA-----	GGCGCTGGGGAGACAGCTA	GTGGAGTACTTGGGGCCAGGGAGTCC	357
361	GGTCAACCGTCTCCTCA			376
358	GGTCAACCGTCTCCTCA			373

RESULT 2
 #MS7559
 LOCUS
 DEFINITION
 MMUS7559 363 bp mRNA linear PRI 11-FEB-1998
 Macaca mulatta Ig rearranged heavy chain variable region, anti-RBC
 antibody, mRNA, partial cds.
 U57559
 ACCESSION
 U57559.1 GI:1575065
 KEYWORDS
 Macaca mulatta (thesus monkey)
 Macaca mulatta
 ORGANISM
 SOURCE
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;

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REFERENCE
AUTHORS
1 (Bases 1 to 363)
Andris,J.S., Miller,A.B., Abraham,S.R., Cunningham,S., Roubinet,F.,
Blancher,A. and Capra,J.D.
TITLE
Variable region gene segment utilization in rhesus monkey
hybridomas producing human red blood cell-specific antibodies:
predominance of the VH4 family but not VH4-21 (V4-34)
JOURNAL
Mol. Immunol. 34 (3), 237-253 (1997)
MEDLINE
97368199
PUBMED
9224966
REFERENCE
2 (Bases 1 to 363)
Andris,J.S., Miller,A.B., Abraham,S.R., Cunningham,S., Blancher,A.
and Capra,J.D.
TITLE
Direct Submission
JOURNAL
Submitted (06-MAY-1996) J.S. Andris, Molecular Immunology Center,
University of Texas Southwestern Medical Center, 6000 Harry Hines
Blvd., Dallas, TX 75235-9140, USA
FEATURES
Location/Qualifiers
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61	ACCTGCAGCTGCTCTGTGGAGGCTCTATCAGCGGCTGGTTTTCATCTGGGGCTGGACTCCGCAAG	120
131	CCCCCAGGGAGGAGACTGGAGTGCATTGGACGTATCTCTGTGTACTGTGTGGGGCCACCAAC	190
121	CCCCCAGGGAGGGCTGGAGTGGATTGGGTGTATATCTATGGTAGTAGTGGAGGACCAAC	180
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181	TACAACCGCTCCCTCAAGAAATCGAGTCACTACCATTTCAAAGAAGACAGTCCAGAAGACCAAGTTC	240
251	TCCCTGAAACCTGAACTCTGTGACCGCCGCGACACGGCCCGTGATTACTGTGTCCAGAGAT	310
241	TCCCTGAAGCTGAGCTCTGTGACCGCCGCGACACGGCCCGTGATTACTGTGTGCGAGAGGT	300
311	TGGGCCCAATAGCTGGAACAAACGTAGAGTCTTCGGGGCCAGGGAGTCCCTGGTCAACGTC	370
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371	TCCTCA	376
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[illegible]

KEYWORDS Igm; Igm heavy chain; immunoglobulin mu heavy chain; variable region.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Chiorazzi, N. and Ferrarini, M. Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.

AUTHORS Dono, M., Zupo, S., Leanza, N., Melioli, G., Fogli, M., Melagrana, A., Chiorazzi, N. and Ferrarini, M.

TITLE Heterogeneity of tonsillar subepithelial B lymphocytes, the splenic marginal zone equivalents

JOURNAL J. Immunol. 164 (11), 5596-5604 (2000)

MEDLINE 20281644

PUBMED 10820234

REFERENCE 2 (bases 1 to 363)

AUTHORS Dono, M.

TITLE Direct Submission

JOURNAL Submitted (11-JAN-2000) Dono M., Istituto Nazionale per la Ricerca sul Cancro, Immunologia Clinica, L.go Rosanna Benzi 10- Genova, ITALY

FEATURES source Location/Qualifiers

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DB 1 CAGGTGCAGCTGCAGAGTCCGGCCCGAGAGTGGTGAAGCCTTCGGAGACCTGTGTCCTC 60

QY 71 ACCTGCGCTGTCTGTGGTCTCTCTCAGCAGTAGTAATCTGTGAGTGGGAGCTGGATCCGCCAG 130

DB 61 ACCTGCGCTGTCTGTGGTCTCTCTCAGCAGTAGTAATCTGTGAGTGGGAGCTGGATCCGCCAG 120

QY 131 CCCCCAGGAGGAGTGGAGTGGATTCGACGATCTCTGTGAGTGGTGGGAGCTGGATCCGCCAG 190

DB 121 CCCCCAGGAGGAGTGGAGTGGATTCGACGATCTCTGTGAGTGGTGGGAGCTGGATCCGCCAG 177

QY 191 TACAACCCGTCCTCAAGAGTGGATTCATCAATTTCAACAAGACAGTCCCAAGAACCGATTC 250

DB 178 TACAACCCGTCCTCAAGAGTGGATTCATCAATTTCAACAAGACAGTCCCAAGAACCGATTC 237

QY 251 TCCCTGACCTGAACTCTGTGACCGCCGACACGCGCGTATTACTGTGACGAGAT 310

DB 238 TCCCTGACCTGAGCTCTGTGACCTGCGGACACGCGCGTATTACTGTGACGAGAT 297

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QY 371 TCCTCA 376

DB 358 TCCTCA 363

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LOCUS Human immunoglobulin heavy chain variable region (V4-4b) gene, partial cds.

ACCESSION U80179

VERSION U80179.1 GI:1791200

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 363) Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.

AUTHORS Glas, A.M., Nottenburg, C. and Milner, E.C.

TITLE Analysis of rearranged immunoglobulin heavy chain variable region genes obtained from a bone marrow transplant (BMT) recipient

JOURNAL Clin. Exp. Immunol. 107 (2), 372-380 (1997)

MEDLINE 97182739

PUBMED 9030878

REFERENCE 2 (bases 1 to 363) Glas, A.M., Nottenburg, C. and Milner, E.C.B. Direct Submission

AUTHORS Submitted (29-NOV-1996) Immunology, Virginia Mason Research Center, 1000 Seneca Street, Seattle, WA 98101, USA

JOURNAL

FEATURES source Location/Qualifiers

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ORIGIN

Query Match 71.4%; Score 268.4; DB 9; Length 363;

Best Local Similarity 85.2%; Pred. No. 2.6e-64;

Matches 312; Conservative 0; Mismatches 51; Indels 3; Gaps 1;

QY 11 CAGCTGCAGCTGCAGAGTCCGGCCCGAGAGTGGTGAAGCCTTCGGAGACCTGTGTCCTC 70

DB 1 CAGGTGCAGCTGCAGAGTCCGGCCCGAGAGTGGTGAAGCCTTCGGAGACCTGTGTCCTC 60

QY 71 ACCTGCGCTGTCTGTGGTCTCTCTCAGCAGTAGTAATCTGTGAGTGGGAGCTGGATCCGCCAG 130

DB 61 ACCTGCGCTGTCTGTGGTCTCTCTCAGCAGTAGTAATCTGTGAGTGGGAGCTGGATCCGCCAG 120

QY 131 CCCCCAGGAGGAGTGGAGTGGATTCGACGATCTCTGTGAGTGGTGGGAGCTGGATCCGCCAG 190

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QY 371 TCCTCA 376
Db 358 TCCTCA 363

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DEFINITION Homo sapiens mRNA for immunoglobulin mu heavy chain variable region, partial cds.
ACCESSION AJ279520
VERSION 1
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Dono, M., Zupo, S., Leanza, N., Melioli, G., Fogli, M., Melagrana, A., Chiorazzi, N. and Ferrarini, M.
Heterogeneity of tonsillar subepithelial B lymphocytes, the splenic marginal zone equivalents
J. Immunol. 164 (11), 5596-5604 (2000)
20281644
PUBMED 10820234
REFERENCE 2 (bases 1 to 366)
Dono, M.
Direct Submission
Submitted (11-JAN-2000) Dono M., Istituto Nazionale per la Ricerca sul Cancro, Immunologia Clinica, L.go Rosanna Benzi 10- Genova, ITALY

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Db 1 CAGGTGCACTGCAAGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCCCTGTGTCCTC 60
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QY 131 CCCCAGGGAAGGAGCTGAGTGGATTGACAGCTATCTCTGGTAGTGGTGGGCCACCAAC 190
Db 121 CCCCAGGGAAGGAGCTGAGTGGATTGAGTGGGAAATCTATCATA--GTGGAGCACCAAC 177
QY 191 TACAACCCGTCCTCAAGAGTCAGTATCATTTTCAAGACACAGTCCTCAAGAACCAAGTTC 250
Db 178 TACAACCCGTCCTCAAGAGTCAGTATCATTTTCAAGACACAGTCCTCAAGAACCAAGTTC 237
QY 251 TCCTGAACTGAACCTCTGTGACCGCGGACACGCGCTGTATTACTGTGTCACAGAT 310
Db 238 TCCTGAACTGAACCTCTGTGACCGCGGACACGCGCTGTATTACTGTGTCACAGAT 297
QY 311 TGGGCCCCAAAT---AGCTGGAAACAGCTAGGCTTCTGGGCCCCAGGAGTCTTGTCAC 367
Db 298 ATGGCGATTTTGGAGTGGTTATTATTTCCGGTACTGGGGCCAGGAAACCCCTGTGTCAC 357
QY 368 GTCTCTCA 376
Db 358 GTCTCTCA 366

RESULT 6
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LOCUS HSU80180
DEFINITION Human immunoglobulin heavy chain variable region (V4-4b) gene, partial cds.
ACCESSION U80180
VERSION 1
KEYWORDS U80180.1 GI:1791202
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 368)
Glas, A.M., Nottenburg, C. and Milner, E.C.
Analysis of rearranged immunoglobulin heavy chain variable region genes obtained from a bone marrow transplant (BMT) recipient
Clin. Exp. Immunol. 107 (2), 372-380 (1997)
97182739
PUBMED 9030878
REFERENCE 2 (bases 1 to 368)
Glas, A.M., Nottenburg, C. and Milner, E.C.B.
Direct Submission
Submitted (29-NOV-1996) Immunology, Virginia Mason Research Center, 1000 Seneca Street, Seattle, WA 98101, USA

FEATURES
source Location/Qualifiers
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Best Local Similarity 85.7%; Pred. No. 8.6e-63;
Matches 318; Conservative 0; Mismatches 45; Indels 8; Gaps 2;

QY 11 CAGCTGCAGCTCAGAGAGTCGGGCCCCGAGGAGTGGTGAAGCCTTCGGAGACCTGTGCCCTC 70
Db 1 CAGGTGCAGCTCAGAGAGTCGGGCCCCGAGGAGTGGTGAAGCCTTCGGAGACCTGTGCCCTC 60

QY 71 ACCTGCGCTGTCTCTGGTGGCTCTGTGCAGCAGTAGTAACCTGTGACCTGGATCGCCAG 130
Db 61 ACCTGCGCTGTCTCTGGTGGCTCTGTGCAGCAGTAGTAACCTGTGACCTGGATCGCCAG 120

QY 131 CCCCAGGAGGAGGAGTGGAGTGGATTCATCTCTGGTAGTGGTGGGCGCACCAAC 190
Db 121 CCCCAGGAGGAGGAGTGGAGTGGATTCATCTCTGGTAGTGGTGGGCGCACCAAC 177

QY 191 TACAACCCGCTCCCTCAAGAGTCGAGTCATCATTTCAAGACACAGCTCCAGAACCCAGTTC 250
Db 178 TACAACCCGCTCCCTCAAGAGTCGAGTCATCATTTCAAGACACAGCTCCAGAACCCAGTTC 237

QY 251 TCCCTGAACCTGAATCTGTGACCGCGCGGACACGCGGTATTAATCTGTGCGCAGAGAT 310
Db 238 TCCCTGAACCTGAATCTGTGACCGCGCGGACACGCGGTATTAATCTGTGCGCAGAGAT 297

QY 311 TGG-----GCCCAATAGCTGGAACAACTAGGCTCTGGGCGCGAGGAGTCCTGGTCA 365
Db 298 AGGTAATTGTAGTAGTACCAAGCTGCANAAATTGACTACTGGGCGCGAGGAGTCTGGTCA 357

QY 365 CGTGTCTCTCA 376
Db 358 CGTGTCTCTCA 368

RESULT 7

HSA245032 363 bp mRNA linear PRI 01-JUN-2000
LOCUS
DEFINITION Homo sapiens mRNA for immunoglobulin mu heavy chain variable region, partial, clone 1-F24.

ACCESSION AJ245032
VERSION
KEYWORDS IGM; IGM heavy chain; immunoglobulin mu heavy chain; variable region.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 Dono, M., Zupo, S., Leanza, N., Melioli, G., Fogli, M., Melagrana, A., Chiorazzi, N. and Ferrarini, M.

TITLE Heterogeneity of tonsillar subepithelial B lymphocytes, the splenic marginal zone equivalents

J. Immunol. 164 (11), 5596-5604 (2000)

JOURNAL

MEDLINE 20281644

PUBMED 10820234

REFERENCE

2 (bases 1 to 363)

Dono, M.

TITLE Direct Submission
Submitted (24-MAY-1999) Dono M., Istituto Nazionale per la Ricerca sul Cancro, Immunologia Clinica, L.go Rosanna benzi 10- Genova, ITALY

FEATURES

source

Location/Qualifiers

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QY 71 ACCTGCGCTGTCTCTGGTGGCTCTGTGCAGCAGTAGTAACCTGTGCGAAGCTGTGATCGCCAG 130
Db 61 ACCTGCGCTGTCTCTGGTGGCTCTGTGCAGCAGTAGTAACCTGTGCGAAGCTGTGATCGCCAG 120

QY 131 CCCCAGGAGGAGGAGTGGAGTGGATTCATCTCTGGTAGTGGTGGGCGCACCAAC 190
Db 121 CCCCAGGAGGAGGAGTGGAGTGGATTCATCTCTGGTAGTGGTGGGCGCACCAAC 177

QY 191 TACAACCCGCTCCCTCAAGAGTCGAGTCATCATTTCAAGACACAGCTCCAGAACCCAGTTC 250
Db 178 TACAACCCGCTCCCTCAAGAGTCGAGTCATCATTTCAAGACACAGCTCCAGAACCCAGTTC 237

QY 251 TCCCTGAACCTGAATCTGTGACCGCGCGGACACGCGGTATTAATCTGTGCGCAGAGAT 310
Db 238 TCCCTGAACCTGAATCTGTGACCGCGCGGACACGCGGTATTAATCTGTGCGCAGAGAT 297

QY 311 TGGGCCCCAATAGCTGGAACAACTAGGCTCTGGGCGCGAGGAGTCCTGGTCAACCGTC 370
Db 298 GAGTATAGCAGCAGATTCACCTGGTTCGACCCCTGGGCGCGAGGAGTCCTGGTCAACCGTC 357

QY 371 TCCTCA 376
Db 358 TCCTCA 363

RESULT 8

HSA279522

LOCUS

DEFINITION Homo sapiens mRNA for immunoglobulin mu heavy chain variable region, partial, clone CD271ow-12.

ACCESSION AJ279522

VERSION

KEYWORDS IGM; IGM heavy chain; immunoglobulin mu heavy chain; variable region.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 Dono, M., Zupo, S., Leanza, N., Melioli, G., Fogli, M., Melagrana, A., Chiorazzi, N. and Ferrarini, M.

TITLE Heterogeneity of tonsillar subepithelial B lymphocytes, the splenic marginal zone equivalents

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region, partial, clone 3-AI.
AU244946
AJ224946.1 GI:4995351
IGM; IGM heavy chain; immunoglobulin mu heavy chain, variable
region.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Dono, M., Zupo, S., Leanza, N., Melioli, G., Fogli, M., Melagrana, A.,
Chiorazzi, N. and Ferrarini, M.
Heterogeneity of tonsillar subepithelial B lymphocytes, the splenic
marginal zone equivalents
J. Immunol. 164 (11), 5596-5604 (2000)
20281644
10820234
PUBMED
REFERENCES   2 (bases 1 to 363)
AUTHORS     Dono, M.
TITLE       Direct Submission
SUBMITTED   (24-MAY-1999) Dono M., Istituto Nazionale per la Ricerca
sul Cancro, Immunologia Clinica, L.go Rosanna benzi 10- Genova,
ITALY
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DB 1 CAGGTGCAGCTCCAGAGTCGGGCCCGACGAGTCGTAAGCCCTTCGGGAGCCCTGTCCCCTC 60
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DB 61 ACCTCGCGTGTCTCTGTGGTGGCTCCATCAGCAGTAGTAATCTGTGGAATTGGGTTCGCCAAG 120
QY 131 CCCCCAGGGAAGGGACTGAGTCGAGTCGAACTCGAACCTCTCTGTGTAGTGTGGTGGGCCACCAAC 190
DB 121 CCCCCAGGGAAGGGGCTGAGTCGAGTCGAAATTGGGGAATCTATCATATA---GTGGGAGCACCAAC 177
QY 191 TACAACCCGCTCCCTCAAGAAGTCGAGTCATCATTTTCAAGAAGCACGTCCTCAAGAACCAAGTTC 250
DB 178 TACAACCCGCTCCCTCAAGAGTCGAGTCACCATATCAGTAGACAAGTCCAAGAACCAAGTTC 237
QY 251 TCCTCGAACCTGAATCTGTGTACCGCCGGGACAGCGCCGTGTATTACTGTGCCAGAGAT 310
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QY 311 TGGGCCCAATAGCTGGAAACAACGCTAGGCTCTGGGGCCAGGAGTCTGGTCCACGCTC 370
DB 298 GAGTGGTTAGCGCTTGTACGGTATGGACGCTCTGGGGCCAGGACCACGGTACCGCTC 357
QY 371 TCCTCA 376
DB 358 TCCTCA 363

RESULT 10
HSA279549 363 bp DNA linear PRI 01-JUN-2000
LOCUS Homo sapiens DNA for immunoglobulin heavy chain variable region,
DEFINITION partial, clone IGM-only-16.
ACCESSION AJ279549
VERSION AJ279549.1 GI:6723593
KEYWORDS immunoglobulin heavy chain; variable region; VH4 family.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE Chiorazzi, N., and Ferrarini, M.
JOURNAL Heterogeneity of tonsillar subepithelial B lymphocytes, the splenic
MEDLINE marginal zone equivalents
PUBMED J. Immunol. 164 (11), 5596-5604 (2000)
REFERENCE 2 (bases 1 to 363)
AUTHORS Dono, M.
TITLE Direct Submission
JOURNAL Submitted (11-JAN-2000) Dono M., Istituto Nazionale per la Ricerca
sul Cancro, Immunologia Clinica, L.go Rosanna Benzi 10- Genova,
ITALY

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QY 71 ACCTCGGCTGTCTCTGGTGGCTCTCTCAGCAGTAGTACTGCTGGAGCCTGGATCCGCCAG 130

DB 61 ACCTGGGCTGTCTCTGGTGGCTCCATCAGCAGTAGTAACCTGGTGGAGTTGGGTCCGCCAG 120
QY 131 CCCCCAGGGAAGGAGCTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGGCCACCAAC 190
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QY 191 TACAACCCGCTCCTCAAGAGTCGAGTCATCAATTCACAAGACACGTCCTCAGAACCCAGTTC 250
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QY 251 TCCTCGAACCTGAACCTCTGTGACCGCGCGGACACGCGCGCTGTATTACTGTGCGAGAGAT 310
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DB 298 GAGTGGTTAGCGCTTGTACGGTATGGACGCTCTGGGGCCAGGACCACGGTACCGCTC 357
QY 371 TCCTCA 376
DB 358 TCCTCA 363

RESULT 11
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LOCUS Human immunoglobulin heavy chain variable region (V4-4b) gene,
DEFINITION partial cds.
ACCESSION U80141
VERSION U80141.1 GI:1791124
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens

REFERENCE 1 (bases 1 to 366)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE Glas, A.M., Nottenburg, C. and Milner, E.C.
JOURNAL Analysis of rearranged immunoglobulin heavy chain variable region
MEDLINE genes obtained from a bone marrow transplant (BMT) recipient
PUBMED Clin. Exp. Immunol. 107 (2), 372-380 (1997)
REFERENCE 2 (bases 1 to 366)
AUTHORS Glas, A.M., Nottenburg, C. and Milner, E.C.B.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-1996) Immunology, Virginia Mason Research Center,
1000 Seneca Street, Seattle, WA 98101, USA

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66 in reference 1"
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ORIGIN

Query Match 67.6%; Score 254; DB 9; Length 375;
Best Local Similarity 84.7%; Pred. No. 2.8e-60;
Matches 310; Conservative 0; Mismatches 50; Indels 6; Gaps 2;
QY 11 CAGCTGCAGCTCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGACCCCTGTCCCTC 70
|||
Db 1 CAGGTGCAGCTCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGACCCCTGTCCCTC 60
QY 71 ACTTGGGCTCTCTGGTGGCTCTGTACAGAGTAGTAACTGTGTGACCTGGATCCGCCAG 130
|||
Db 61 ACTTGCACCTGTCTCTGGTGGCTCTGTACAGAGTAGTAACTGTGTGACCTGGATCCGCCAG 120
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Db 121 CCCCCAGGAGGAGCTGAGGAGTGGATGGAGCTATCTCTGGTGGTGGGCGCCACCTAC 177
QY 191 TACACCCCTCCTCAAGAGTCAGTGCATATTTCAAGAGACGTCGACGTCGAGGTC 250
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Db 178 TACACCCCTCCTCAAGAGTCAGTGCATATTTCAAGAGACGTCGACGTCGAGGTC 237
QY 251 TCCTGAACCTGAACCTCTGTGACCGCGCGGACACGCGGTGTATTACTGTGCCAGAGAT 310
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Db 238 TCCTGAACCTGAGCTCTGTGACCGCGCGGACACGCGGTGTATTACTGTGCCAGAGAT 297
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QY 371 TCCTCA 376
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Db 355 TCCTCA 360

RESULT 14
AY376082
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DEFINITION Homo sapiens isolate VH-CE-A54 immunoglobulin E heavy chain
variable region mRNA, partial cds.
ACCESSION AY376082
VERSION AY376082.1 GI:37014228
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Davies, J.M. and O'Hehir, R.E.
TITLE VH gene usage in IgE responses of grass pollen allergic individuals
is oligoclonal and antigen driven
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 364)
AUTHORS Davies, J.M. and O'Hehir, R.E.
TITLE Direct Submission
JOURNAL Submitted (28-AUG-2003) Allergy, Immunology and Respiratory
Medicine, The Alfred Hospital, Commercial Road, Melbourne, VIC

3004, Australia
Location/Qualifiers
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Db 2 AGGTGCAGCTGCTCGAGTTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGACCCCTGTCCCTCA 61
QY 72 CCTGGCTGTCTCTGGTGGCTCTGTACAGAGTAGTAACTGTGTGACCTGGATCCGCCAGC 131
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QY 132 CCCCAGGAGGAGGAGCTGAGTGGATGGAGCTATCTCTGGTGGTGGGCGCCACCAACT 191
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Db 122 CCCCAGGAGGAGGAGCTGAGTGGATGGAGCTATCTCTGGTGGTGGGCGCCACCTCT 178
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Db 299 GGGAGAGACTACGCGGCGGAGGATTTGACTACTTGGGCGCAGGAGAACCTGTGTCACCGGTC 358
QY 372 CCTCA 376
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Db 359 CCTCA 363

RESULT 15
HSA556684
LOCUS HSA556684
DEFINITION Homo sapiens partial mRNA for immunoglobulin gamma heavy chain
variable region (IGHV4-04 gene), clone IA-4G 019.
ACCESSION AJ556684.1
VERSION AJ556684.1 GI:31337609
KEYWORDS IGHV4-04 gene; immunoglobulin gamma heavy chain; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Colombo, M., Dono, M., Gazzola, P., Chiorazzi, N., Mancardi, G. and
Ferrarini, M.
TITLE Maintenance of B lymphocytes related clones in the cerebrosplinal
fluid of multiple sclerosis patients
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 363)
AUTHORS Colombo, M.
TITLE Direct Submission

JOURNAL Submitted (26-FEB-2003) Colombo M., Medical Oncology C. IST-IST.
Nazione. Ricerca Cancro, Largo Rosanna Benzi 10, Genova 16132, ITALY

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Query Match 67.1%; Score 252.4; DB 9; Length 363;
Best Local Similarity 82.5%; Pred. No. 8e-60;
Matches 302; Conservative 0; Mismatches 61; Indels 3; Gaps 1;
Qy 11 CAGCTGACCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTC 70
Db |||||
Qy 1 CAGCTGACCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTC 60
Db |||||
Qy 71 ACCTGCGCTGTCTCTGTGGCTCTGTCTGACGAGTAGTAACTGGTGGACCTGGATCCGCCAG 130
Db |||||
Qy 61 ACCTGCGCTGTCTCTGTGGCTCTGTCTGACGAGTAGTAACTGGTGGACCTGGATCCGCCAG 120
Db |||||
Qy 131 CCCCAGGGAAGGAGCTGGAGTGGATGGACGTATCTCTGTGTAGTGGGGCCACCAC 190
Db |||||
Qy 121 CCCCAGGGAAGGAGCTGGAGTGGATGGAGAAATCTATCATA---GTGGAGACCCAGG 177
Db |||||
Qy 191 TACAAACCGTCCCTCAAGAGTCGAGTCAATCTTCAAGACACGTCACAGAACCACTTC 250
Db |||||
Qy 178 TACAAACCGTCCCTCAAGAGTCGAGTCAATCTTCAAGACACGTCACAGAACCACTTC 237
Db |||||
Qy 251 TCCCTGAACCTGAACCTGTGACCGCCGACACCGCGGTGATTAATCTGTGCCAGAGAT 310
Db |||||
Qy 238 TCCCTGAACCTGAACCTGTGACCGCCGACACCGCGGTGATTAATCTGTGCCAGAGAT 297
Db |||||
Qy 311 TGGGCCCAATAGCTGGAAACACGCTGTCTGGGGCCAGGAGTCCTGGTCCACCGTC 370
Db |||||
Qy 298 AGTTTCTATGATAGCGGGGGTGTCTTTTGTATCTGGGGCCAGGACAAATGGTCCCGTC 357
Db |||||
Qy 371 TCCTCA 376
Db |||||
Qy 358 TCTTCA 363

Search completed: June 19, 2004, 07:02:22
Job time : 1848 secs


```
CC an epitope in domain 5 of trkC. The antibodies of the invention are
CC effective in the treatment of cisplatin- or pyridoxine-induced
CC neuropathy, peripheral neuropathy, diabetic neuropathy and large-fibre
CC sensory neuropathy, neurodegenerative disease including amyotrophic
CC lateral sclerosis, nerve cell injuries, disorders of insufficient blood
CC cells such as leukopenia including eosinopenia, basopenia,
CC lymphopenia, monocytopenia, neutropenia, Alzheimer's disease,
CC Parkinson's disease, Huntington's disease and tumours. The sequences are
CC also useful for inducing angiogenesis for treating wounds, ulcers and
CC diabetic complications of sickle cell disease, for treating cardiac
CC ischaemia and cerebrovascular disorders and in the diagnosis of diseases
CC involving cellular degeneration. Sequences ABK24399-ABK24413 represent
CC DNA molecules encoding human and mouse anti-trkC agonist monoclonal
CC antibodies and antibody fragments of the invention
XX
SQ Sequence 354 BP; 73 A; 107 C; 103 G; 71 T; 0 U; 0 Other;

Query Match          64.7%; Score 243.2; DB 6; Length 354;
Best Local Similarity 85.0%; Pred. No. 1.6e-57;
Matches 311; Conservative 0; Mismatches 43; Indels 12; Gaps 3;

QY 11 CAGCTGAGCTGCAGAGTGGGGCCAGAGTGGTGAAGCTTCGGAGACCTTCCTCCTC 70
Db 1 CAGGTGACAGTGCAGAGTGGGGCCAGAGTGGTGAAGCTTCGGAGACCTTCCTCCTC 60

QY 71 ACCTGGCTGTCTCTGGTGGCTCTGTACAGCAGTGTAACTGTGTGACCTGGATCCGACG 130
Db 61 ACCTGCATCTCTCTGGTGGCTC---CATCAGTACTTACTGTGAAGTGAATCCGGCAG 117

QY 131 CCCCAGGAGGAGCTGAGTGTGAGTGTGAAGTATCTCTGTGTAGTGTGGGGCCACCAAC 190
Db 118 CCGCGGGAAGGAGTGTGAGTGTGAGTGTGGGTATCT---ATACAGTGGGAGCACCAC 174

QY 191 TACAACCGCTCCCTCAAGAGTCGAGTCATCTTTCACAGACACGTCCTCAAGAACCAAGTTC 250
Db 175 TACAACCGCTCCCTCAAGAGTCGAGTCATCTTTCACAGACACGTCCTCAAGAACCAAGTTC 234

QY 251 TCCCTGAACCTGAACCTGTGTACCGCCCGGACACCGCCGTGTATTACTGTGCGAGAGAT 310
Db 235 TCCCTGAAGCTGAGCTGTGTACCGCCCGGACACCGCCGTGTATTACTGTGCGAGAGAT 294

QY 311 TGGGCCCCAATAGCTGGAGAACCGTAGGCTTCTGGGGCCAGGAGTCTGTGTCACCGTC 370
Db 295 GGGGGCTACA-----GTAAACCTTTTACTGTGGGGCCAGGAGCCCTGTGTCACCGTC 348

QY 371 TCCTCA 376
Db 349 TCCTCA 354

RESULT 2
AAT45035
XX ID AAT45035 standard; cDNA; 372 BP.
XX AC AAT45035;
XX
XX 23-MAY-1997 (first entry)
XX
XX Human lung cancer specific antibody heavy chain variable region cDNA.
XX
XX Heavy chain; light chain; variable region; human; monoclonal antibody;
XX lung cancer tissue; diagnosis; purification; cancer-specific antigen; ss.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT misc_RNA 91..108
XX FT /*tag= a
XX FT /product= "CDR1"
XX FT /note= "Fig 5, Claim 7"
XX FT misc_difference 139..141
XX FT /*tag= b
XX FT /codon= seq:gag, aa:Gln
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```
FT misc_RNA 151..198
FT FT /*tag= c
FT FT /product= "CDR2"
FT FT /note= "Fig 6, Claim 7"
FT FT 295..339
FT FT /*tag= d
FT FT /product= "CDR3"
FT FT /note= "Fig 7, Claim 7"
XX
XX JP08280386-A.
XX
XX 29-OCT-1996.
XX
XX 14-APR-1995; 95JP-00112671.
XX
XX 14-APR-1995; 95JP-00112671.
XX
XX (MOMI ) MORINAGA & CO LTD.
XX
XX WPI: 1997-014849/02.
XX P-PSDB; AAW06474.
XX
XX Antibody specifically reactive to human lung cancer cells - also
XX corresponding DNA, used to diagnose cancer, or for purification of cancer
XX -specific antigen.
XX
XX Claim 1; Fig 1; 9pp; Japanese.
XX
XX The sequences given in AAT45035-36 encode the heavy chain and light chain
XX variable regions from a human monoclonal antibody which is specific for
XX human lung cancer tissue. The monoclonal antibody may be used for
XX clinical diagnosis of cancers, for immunological therapy or for
XX purification of a cancer-specific antigen
XX
XX Sequence 372 BP; 77 A; 102 C; 117 G; 76 T; 0 U; 0 Other;

Query Match          64.6%; Score 243; DB 2; Length 372;
Best Local Similarity 82.1%; Pred. No. 1.8e-57;
Matches 308; Conservative 0; Mismatches 55; Indels 12; Gaps 2;

QY 11 CAGCTCAGCTGCAGAGTGGGGCCAGAGTGGTGAAGCTTCGGAGACCTTCCTCCTC 70
Db 1 CAGGTGACAGTGCAGAGTGGGGCCAGAGTGGTGAAGCTTCGGAGACCTTCCTCCTC 60

QY 71 ACCTGGCTGTCTCTGGTGGCTCTGTACAGCAGTGTAACTGTGTGACCTGGATCCGACG 130
Db 61 ACCTGGCTGTCTCTGGTGGCTCCTCATCAGCAGTGTAACTGTGTGAGTGGGTCCGCCAG 120

QY 131 CCCCAGGAGGAGCTGGAGTGGATTGGACCTGTCTCTGTGTAGTGTGGGGCCACCAAC 190
Db 121 CCCCAGGAGGAGGAGCTGGAGTGGATTGGAGTGGATTGGGAAATCTATCATA---GTGGAGACCAAC 177

QY 191 TACAACCGCTCCCTCAAGAGTGCAGTGCATCTTTCACAGACACGTCCTCAAGAACCAAGTTC 250
Db 178 TATAACCGCTCCCTCAAGAGTGCAGTGCATCTTTCACAGACACGTCCTCAAGAACCAAGTTC 237

QY 251 TCCCTGAACCTGAACCTGTGTACCGCCCGGACACCGCCGTGTATTACTGTGCGCAGA--- 307
Db 238 TCCCTGAAGTGAACCTGTGTACCGCCCGGACACCGCCGTGTATTACTGTGCGGAGAG 297

QY 308 -----GATTGGGGCCCAATAGCTGGAAACAACGCTAGGCTTCTGGGGCCAGGAGTCTG 361
Db 298 AATTACGATTTTGGAGTGGTGGCGAGCGGCCCATTTGACTACTGGGGCCAGGAGCGCTG 357

QY 362 GTCACCGTCTCTCA 376
Db 358 GTCACCGTCTCTCA 372

RESULT 3
ABS57441
XX ID ABS57441 standard; cDNA; 360 BP.
```


KW	Multiple sclerosis; cerebrospinal fluid; CSF; B-cell;	
KW	heavy chain variable region; VH gene; somatic hypermutation;	
KW	B-cell clonality; ML gene; diagnosis; human; ss.	
XX		
OS	Homo sapiens.	
XX		
XX		
Key	Location/Qualifiers	
CD5	1..234	
FT	/*tag= s	
FT	/transl_except= (pos:16..18, aa:Gly)	
FT	replace(15,A)	
FT	/*tag= b	
FT	/note= "mutation in FR1 compared with ML"	
FT	replace(19,T)	
FT	/*tag= a	
FT	/note= "mutation in FR1 compared with ML"	
FT	replace(75,G)	
FT	/*tag= c	
FT	/note= "mutation in FR1 compared with ML"	
FT	replace(78,A)	
FT	/*tag= d	
FT	/note= "mutation in FR1 compared with ML"	
FT	replace(163,G)	
FT	/*tag= e	
FT	/note= "mutation in CDR2 compared with VL"	
FT	replace(170,C)	
FT	/*tag= f	
FT	/note= "mutation in CDR2 compared with ML"	
FT	replace(176,G)	
FT	/*tag= g	
FT	/note= "mutation in CDR2 compared with ML"	
FT	replace(177,G)	
FT	/*tag= h	
FT	/note= "mutation in CDR2 compared with ML"	
FT	replace(163,T)	
FT	/*tag= i	
FT	/note= "mutation in CDR2 compared with ML"	
FT	replace(185,T)	
FT	/*tag= r	
FT	/note= "mutation in FR3 compared with ML"	
FT	replace(214,A)	
FT	/*tag= j	
FT	/note= "mutation in FR3 compared with ML"	
FT	replace(221,G)	
FT	/*tag= k	
FT	/note= "mutation in FR3 compared with ML"	
FT	replace(232,A)	
FT	/*tag= l	
FT	/note= "mutation in FR3 compared with ML"	
FT	replace(234,T)	
FT	/*tag= m	
FT	/note= "mutation in FR3 compared with ML"	
FT	replace(249,C)	
FT	/*tag= n	
FT	/note= "mutation in FR3 compared with ML"	
FT	replace(251,A)	
FT	/*tag= o	
FT	/note= "mutation in FR3 compared with ML"	
FT	replace(252,G)	
FT	/*tag= p	
FT	/note= "mutation in FR3 compared with ML"	
FT	replace(284,T)	
FT	/*tag= q	
FT	/note= "mutation in FR3 compared with ML"	
XX		
XX	WO9915696-A1.	
XX		
XX	01-APR-1999.	
XX		
XX	17-SEP-1998;	98WO-CAD000873.
XX		
XX	19-SEP-1997;	97CA-02216595.
PR	04-NOV-1997;	97CA-02220245.

XX	(QIN Y/) QIN Y.
PA	Qin Y;
PI	WPI: 1999-276985/23.
XX	P-PDOB; AAY05693.
DR	Determination of B-cell clonality by amplification or enzymatic digestion.
XX	Disclosure; Fig 9B; 67pp; English.
PS	This is the nucleotide sequence of the heavy chain variable region (VH) gene from a dominant clone, termed 4d68, of B-cells taken from the cerebrospinal fluid (CSF) of a multiple sclerosis (MS) patient. Sequences of VH of CSF B-cells were obtained from 4 MS patients (see AAX25316-19).
CC	Differences in nucleotide and predicted amino acid (see AAY05691-94) sequences were compared with the closest known germline VH genes; for 4d68, this was ML. The results provided direct evidence that intrathecal clonally expanded B-cells from the CSF of MS patients are hypermutated postgerminal centre antibody-forming or memory lymphocytes that have undergone antigen selection. This finding implicates an important pathogenic pathway for the development of demyelination in CNS of MS. The invention provides assay kits for determining B-cell or T-cell clonality. This technology allows the establishment of clonal specific RNA library from pathogenic cells in the CNS of patients, which is important for further understanding of the role of antigen(s) in the cause of B-cell clonal expansion, and towards developing antigen specific therapeutic strategy
XX	Sequence 294 BP; 62 A; 84 C; 91 G; 57 T; 0 U; 0 Other;
SQ	Query Match 64.1%; Score 241; DB 2; Length 294; Best Local Similarity 90.6%; Pred. NO. 6.2e-57; Matches 269; Conservative 0; Mismatches 25; Indels 3; Gaps 1;
QY	11 CAGCTGCAGCTGCGAGAGTCGGGCCCAGAGGTGTTGAAGCCTTTCGGAGACCTGTGTCCCTC 70
Db	1 CAGGTGCAGCTGCAGAGGTGCGGCCCCAGACTGTGTGAAGCCTTTCGGGACCCTGTGTCCCTC 60
QY	71 ACCTGCCTGTCTCTGGTGCTCTGTCAACAGTAGTAACCTGTGACCTGTATCGGCAG 130
Db	61 ACCTGCCTGTCTCTGGTGCTCTCATCACAGTAGTAACCTGTGTGAGTGTGGTTCGGCCAG 120
QY	131 CCCCCAGGAAGGAGCTGGAGTGCATTGGACCTATCTCTGGTAGTGTGGGGCCACCACAAC 190
Db	121 CCCCCAGGAAGGGCTGGAGTGGATTGGGAAATCTATCATATA---GTGGGAGCACCAAC 177
QY	191 TACAACCGCTCCTCAAGAGTGCAGTGCATCTTTCACAAGACACAGTTCOAAGAACAAGTTTC 250
Db	178 TACAACCGCTCCTCAAGAGTGCAGTGCATCTTTCACAAGACACAGTTCOAAGAACAAGTTTC 237
QY	251 TCCTCTGAACCTGAACTCTGTGACCGCGCGGACAGCGCGGTGTATTACTGTGGCAGA 307
Db	238 TCCTCTGAAGCTGAGCTCTGTGACCGCGCGGACAGCGCGGTGTATTACTGTGGCAGA 294
RESULT 7	
ID	ABSG62723 standard; DNA; 358 BP.
AC	ABSG62723;
XX	24-OCT-2002 (first entry)
XX	Anti-IGF-IR antibody VH chain DNA consensus sequence #2.
XX	Insulin-like growth factor I receptor; antibody; human; ds; gene;
KW	cystostatic; osteopathic; antiatherosclerotic; antipsoriatic; IGF-IR;
KW	tumour; anti-neoplastic; anti-tumour; anti-angiogenic; neuropathy;
XX	osteoporosis; acromegaly; gigantism; psoriasis; atherosclerosis.
XX	

OS Homo sapiens.
 XX WO200253596-A2.
 PN 11-JUL-2002.
 PD 20-DEC-2001; 2001WO-US051113.
 PF 05-JAN-2001; 2001US-0259927P.
 PR (PFIZ) PFIZER INC.
 XX (ABGE-) ARGENIX INC.
 PA Cohen BD, Beebe J, Miller PE, Moyer JD, Corvalan JR, Gallo M;
 XX WPI; 2002-575410/61.
 DR Novel humanized, chimeric monoclonal antibody that specifically binds to
 XX insulin-like growth factor I (IGF-I) receptor useful for inhibiting
 XX binding of IGF-I or IGF-II to receptor and for treating cancer in humans.
 PT Disclosure; Fig 23; 172pp; English.
 PS This invention relates to a novel humanised, chimeric or human monoclonal
 XX antibody or its antigen binding portion that specifically binds to
 CC insulin-like growth factor I receptor (IGF-IR). The antibodies of the
 CC invention can act as an inhibitor of binding of IGF-I or IGF-II with IGF-
 CC IR and can inhibit in vivo tumour growth and IGF-IR tyrosine
 CC phosphorylation. The antibodies of the invention are useful for
 CC diagnosing the presence or location of an IGF-IR-expressing tumour in a
 CC subject. The antibody or its antigen-binding portion is also useful for
 CC treating cancer in a human. The method for this further involves an anti
 CC neoplastic, anti-tumour, anti-angiogenic or chemotherapeutic agent. The
 CC antibodies may also be useful for increasing IGF-IR activity and thus
 CC restoring IGF-IR activity in a condition characterised by low IGF-IR
 CC levels e.g. neuropathy, or osteoporosis. An antibody of the invention is
 CC also useful for inducing apoptosis of specific cells in a patient, and to
 CC treat non-cancerous states or disease, e.g. acromegaly, gigantism,
 CC psoriasis and atherosclerosis. Fully human anti-IGF-IR antibodies
 CC minimise the immunogenic and allergic responses intrinsic to mouse or
 CC mouse-derived monoclonal antibodies and thus increase the efficacy
 CC and safety of the administered antibodies. The present sequence
 CC represents a DNA sequence encoding an anti-insulin-like growth factor I
 CC receptor antibody of the invention
 XX
 SQ Sequence 358 BP; 70 A; 103 C; 101 G; 79 T; 0 U; 5 Other;
 Query Match 62.6%; Score 235.4; DB 6; Length 358;
 Best Local Similarity 82.5%; Pred. No. 2.3e-55;
 Matches 302; Conservative 4; Mismatches 51; Indels 9; Gaps 3;
 QY 11 CAGCTGCAGCTGCAGGAGTCCGGCCAGGAGTGTGAAGCTTCGGAGACCCCTGTCCCTC 70
 DB 1 CAGGTGCAGCTGCAGGAGTCCGGCCAGGAGTGTGAAGCTTCGGAGACCCCTGTCCCTC 60
 QY 71 ACCTGCGCTGTCTCTGGTGGCTCTGTCTCAGCAGTGTGAAGCTTCGGAGTGTGAAGCTTCGGAG 130
 DB 61 ACCTGCACTGTCTCTGGTGGCTC---CATCAGTATTTACTTGTGAGTGTGAAGCTTCGGAG 117
 QY 131 CCCCAGGAGGAGGAGCTGAGTGTGAAGTGTGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 190
 DB 118 CCCCAGGAGGAGGAGCTGAGTGTGAAGTGTGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 174
 QY 191 TACAAACCGTCCCTCAAGAGTGTGATCATATTTCAAGACAGCTGCAGAACCACTTC 250
 DB 175 TACAAACCGTCCCTCAAGAGTGTGATCATATTTCAAGACAGCTGCAGAACCACTTC 234
 QY 251 TCCCTGAACTTGAATCTGTACCGCCGCGACACCGCGGTGTATTTACTGTGCGAGAT 310
 DB 235 TCCCTGAACTTGAATCTGTACCGCCGCGACACCGCGGTGTATTTACTGTGCG---GATA 291
 QY 311 TGGGCCCAATAGCTGTGAACACGCTAGGCTTCTTGGGGCCAGGAGTCTGTGTCACCGTC 370

Db 292 ACCATTTTGGAGTGGTTATTATCTTGTACTGCGGCGCAGGANCCTGTCCCGTC 351
 QY 371 TCCTCA 376
 DB 352 TCCTCA 357
 RESULT 8
 ABS20941
 ID ABS20941 standard; DNA; 362 BP.
 XX AC ABS20941;
 XX DT 19-AUG-2002 (first entry)
 XX DE Human genome-derived single exon probe ORF from lung SEQ ID No 20932.
 XX KW Human; db; single exon probe; asthma; lung cancer; COPD; ILD;
 KW chronic obstructive pulmonary disease; interstitial lung disease;
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
 KW Hermansky-Rudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
 KW primary ciliary dyskinesia; pulmonary hypertension;
 KW hyaline membrane disease; open reading frame; ORF.
 OS Homo sapiens.
 XX WQ200186003-A2.
 XX PD 15-NOV-2001.
 XX PF 30-JAN-2001; 2001WO-US000665.
 XX PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX (MOLB-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2002-114183/15.
 XX Spatially-addressable set of single exon nucleic acid probes, used to
 PT measure gene expression in human lung samples.
 XX Claim 4; SEQ ID NO 20932; 634pp; English.
 CC The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human lung comprising single exon nucleic acid probes having one of
 CC 12614 nucleic acid sequences mentioned in the specification, or their
 CC complements or the 12387 open reading frames derived from the 12614
 CC probes. Also included are a microarray comprising the novel set of probes
 CC; the novel set of probes which hybridise at high stringency to a nucleic
 CC acid expressed in the human lung; measuring gene expression in a sample
 CC derived from human lung, comprising (a) contacting the array with a
 CC collection of detectably labeled nucleic acids derived from human lung
 CC mRNA, and (b) measuring the label detectably bound to each probe of the
 CC array; identifying exons in a eukaryotic genome, comprising (a)
 CC algorithmically predicting at least one exon from genomic sequences of
 CC the eukaryote; and (b) detecting specific hybridisation of detectably
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 CC having a fragment identical to the predicted exon, the probe is included
 CC in the above mentioned microarray; assigning exons to a single gene,
 CC comprising (a) identifying exons from genomic sequence by the method
 CC above and (b) measuring the expression of each of the exons in several

XX DE Mab 1-3-1 variable region of heavy chain.
XX KW Monoclonal antibody; hybridoma; PCR; variable region; constant region;
XX KW heavy chain; light chain; ss.
XX OS Synthetic.
XX PN EP520499-A1.
XX PD 30-DEC-1992.
XX PF 26-JUN-1992; 92EP-00110841.
XX PR 28-JUN-1991; 91JP-00158859.
XX PR 28-JUN-1991; 91JP-00158860.
XX PR 28-JUN-1991; 91JP-00158861.
XX PA (MITU) MITSUBISHI KASEI CORP.
XX PI Hosokawa S, Tagawa T, Hirakawa Y, Ito N, Nagaike K;
XX WPI; 1993-001328/01.
XX DR P-PSDB; AAR30145.
XX KW Human monoclonal antibody specific for a cancer cell membrane surface
XX PT antigen - prep'd. from a hybridoma obtd. by cell fusion between human
XX PS lymphocytes derived from cancer patients and mouse myeloma cells.
XX PS Claim 17; Page 31 + 18; 37pp; English.
XX CC A human MAb specifically binding to a surface antigen of cancer cell
XX CC membrane comprises variable regions of the heavy and light chains having
XX CC the amino acid sequences of AAR30145-46 respectively, encoded by DNA
XX CC sequences AAQ33035-36 respectively. (Updated on 25-MAR-2003 to correct PN
XX CC field.)
XX SQ Sequence 366 BP; 76 A; 105 C; 111 G; 74 T; 0 U; 0 Other;

Query Match 62.4%; Score 234.6; DB 2; Length 366;
Best Local Similarity 81.0%; Pred. No. 3.9e-55;
Matches 299; Conservative 0; Mismatches 64; Indels 6; Gaps 2;
QY 11 CAGCTGCAGCTGCAGAGTGGGCGCCAGGAGTGTGAAGCTTCGAGACCTGTCCCTC 70
DB 1 CAGCTGCAGCTGCAGAGTGGGCGCCAGGAGTGTGAAGCTTCGAGACCTGTCCCTC 60
QY 71 ACTTGGCTCTCTGTGGTCTGTGTCAGCAGTAGTA---ACTGTGGACCTGGATCCGC 127
DB 61 ACTTGGCTCTCTGTGGTCTGTGTCAGCAGTAGTA---ACTGTGGACCTGGATCCGC 120
QY 128 CAGCCCCAGGAGGAGTGGAGTGGATGGAGTGTCTCTGTGGTGGGCGCAC 187
DB 121 CAGCCCCAGGAGGAGTGGAGTGGATGGAGTGTCTCTGTGGTGGGCGCAC 177
QY 188 AACTACAACCCCTCCCTCAAGAGTGCAGTCAATTTCAAGACACGTCACCAAGACCA 247
DB 178 TACTACAACCCCTCCCTCAAGAGTGCAGTCAATTTCAAGACACGTCACCAAGACCA 237
QY 248 TTCTCCTGAACTGAACTGTGTGACCGCGCGGACACCGCGGTGATTACTGTGCCA 307
DB 238 TTCTCCTGAACTGAACTGTGTGACCGCGCGGACACCGCGGTGATTACTGTGCCA 297
QY 308 GATTGGGCCCAATAGCTGGAACAAGCTAGGCTTCTGGGGCCAGGAGTCTGTGGTCA 367
DB 298 GGGAGCTACGGGGCTTACTACTAGGTATGAGCTGTGGGGCCAGGACCAAGGTCAC 357
QY 368 GTCTCTCA 376
DB 358 GTCTCTCA 366

RESULT 11

AAZ49608/c
ID AAZ49608 standard; DNA; 351 BP.
XX AAZ49608;
XX AC AAZ49608;
XX DT 07-APR-2000 (first entry)
XX DE DNA-1 related to human antibody clone NHS76.
XX KW Human antibody clone NHS76; cytostatic; malignant tumour;
XX KW human histone H1; antibody; intracellular antigen; diagnosis; treatment;
XX KW tumour; cervical; ovarian; prostate; lung; liver; pancreatic; colon;
XX KW stomach; ds.
XX OS Homo sapiens.
XX PN WO200001822-A1.
XX PD 13-JAN-2000.
XX PF 02-JUL-1999; 99WO-GB002123.
XX PR 02-JUL-1998; 98GB-00014383.
XX PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX PI Williams AJ, Tempest PR, Holtet TL, Jackson H;
XX WPI; 2000-137204/12.
XX PT New specific binding members capable of binding an intracellular antigen,
XX PT useful in the treatment and diagnosis of tumors.
XX SQ Disclosure; Page 64; 70pp; English.
XX CC The present DNA sequence is related to human antibody clone NHS76. NHS76
XX CC is useful for targeting the necrotic centres of malignant tumours by
XX CC binding to human histone H1 and other intracellular antigens. The
XX CC specific binding members based on the CDRs (complementarity determining
XX CC regions) of NHS76 can be used in diagnosis and treatment of tumours like
XX CC cervical, ovarian, prostate, lung, liver, pancreatic, colon and stomach
XX CC tumours. Note: There is no relevant information regarding this sequence
XX CC in the specification
XX SQ Sequence 351 BP; 75 A; 103 C; 99 G; 74 T; 0 U; 0 Other;

Query Match 62.3%; Score 234.4; DB 3; Length 351;
Best Local Similarity 82.0%; Pred. No. 4.4e-55;
Matches 300; Conservative 0; Mismatches 51; Indels 15; Gaps 2;
QY 11 CAGCTGCAGCTGCAGAGTGGGCGCCAGGAGTGTGAAGCTTCGAGACCTGTCCCTC 70
DB 351 CAGCTGCAGCTGCAGAGTGGGCGCCAGGAGTGTGAAGCTTCGAGACCTGTCCCTC 292
QY 71 ACCTGCGCTGTCTCTGTGGTCTGTGTCAGCAGTAGTA---ACTGTGGACCTGGATCCGCAG 130
DB 291 ACCTGCGCTGTCTCTGTGGTCTGTGTCAGCAGTAGTA---ACTGTGGACCTGGATCCGCAG 232
QY 131 CCCCCAGGAGGAGTGGAGTGGATGGAGTGTCTCTGTGGTGGGCGCACCAAC 190
DB 231 CCCCCAGGAGGAGGAGTGGAGTGGATGGAGTGTCTCTGTGGTGGGCGCACCTAC 175
QY 191 TACAACCCCTCCCTCAAGAGTGCAGTCAATTTCAAGACACGTCACCAAGACCAAGTTC 250
DB 174 TACAACCCCTCCCTCAAGAGTGCAGTCAATTTCAAGACACGTCACCAAGACCAAGTTC 115
QY 251 TCCCTGAACTGAACTGTGTGACCGCGCGGACACCGCGGTGATTACTGTGCCAGAT 310
DB 114 TCCCTGAACTGAACTGTGTGACCGCGCGGACACACCGCGGTGATTACTGTGCCAGAGG 55
QY 311 TGGGCCCCAAATAGCTGGAACAACCTAGGCTTCTGGGGCCAGGAGTCTGTGGTCAACGTC 370
DB 54 AAG-----TGGTCGAGTTTGACTATTGGGGCCCAAGSCACCTGGTCAACGTC 7


```
QY 371 TCCTCA 376
Db 6 TCCTCA 1

RESULT 12
AAZ49590
ID AAZ49590 standard; DNA; 351 BP.
XX
XX
AC AAZ49590;
XX
XX 07-APR-2000 (first entry)
XX
XX Human antibody clone NHS76 VH gene.
XX
XX Human antibody clone NHS76 VH; VH; heavy chain variable region;
XX cytostatic; malignant tumour; human histone H1; antibody;
XX intracellular antigen; diagnosis; treatment; tumour; cervical; ovarian;
XX prostate; lung; liver; pancreatic; colon; stomach; prodrug; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX 1. 351
XX CDS /*tag= a
XX FT /product= "Human antibody clone NHS76 VH"
XX FT /note= "no stop codon given"
XX
XX PN WO200001822-A1.
XX
XX PD 13-JAN-2000.
XX
XX PF 02-JUL-1999; 99WO-GB002123.
XX
XX PR 02-JUL-1999; 98GB-00014383.
XX
XX PA (CAME-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX PI Williams AJ, Tempest PR, Holtet TL, Jackson H;
XX
XX WPI; 2000-137204/12.
XX
XX DR P-PSDB; AAY44615.
XX
XX New specific binding members capable of binding an intracellular antigen,
XX useful in the treatment and diagnosis of tumors.
XX
XX Claim 15; Fig 1; 70pp; English.
XX
XX The present sequence encodes human antibody clone NHS76 heavy chain
XX variable region. This is useful for targeting the necrotic centres of
XX malignant tumours by binding to human histone H1 and other intracellular
XX antigens. The NHS76 VH gene can be used in the construction of expression
XX vectors. The specific binding members based on the CDRs (complementarity
XX determining regions) of NHS76 can be used in diagnosis and treatment of
XX tumours like cervical, ovarian, prostate, lung, liver, pancreatic, colon
XX and stomach tumours. The antibody is labelled with functional labels such
XX as toxins and enzymes which are capable of converting prodrugs into
XX active drugs at the site of a tumour
XX
XX Sequence 351 BP; 74 A; 99 C; 103 G; 75 T; 0 U; 0 Other;

Query Match 62.3%; Score 234.4; DB 3; Length 351;
Best Local Similarity 82.0%; Pred. No. 4.4e-55;
Matches 300; Conservative 0; Mismatches 51; Indels 15; Gaps 2;

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Db 1 CAGGTGCAGCTGCAGAGTCCGGCCAGGAGTGGTGAAGCTTCGGAGACCTGTGCTC 60
QY 71 ACCTGGCTGTCTGTGGTCTGTCTAGCTAGTACTAGTGGTGGTGGTGGTGGTGGT 130
Db 61 ACCTGGCTGTCTGTGGTCTGTCTAGCTAGTACTAGTGGTGGTGGTGGTGGTGGT 120
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2004, 06:22:06 ; Search time 63 seconds
(without alignments)
3312.088 Million cell updates/sec

Title: US-09-019-441a-3_COPY_48_423

Perfect score: 376
Sequence: 1 ggcctgtccagctgcagc.....tctgtgacccgtctctca 376

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1068194

Minimum DB seq length: 0
Maximum DB seq length: 376

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*
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2: /cgn2_6/ptodata/2/ins/5B_COMB.seq.*
3: /cgn2_6/ptodata/2/ins/6A_COMB.seq.*
4: /cgn2_6/ptodata/2/ins/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ins/PCRUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ins/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	237.8	63.2	366	1	US-08-360-125-9
2	237.8	63.2	366	2	US-08-450-578-9
3	237.8	63.2	366	2	US-09-017-628-9
4	237.8	63.2	366	2	US-09-014-880-9
5	237.8	63.2	366	4	US-08-450-363-9
6	217.6	57.9	372	2	US-08-477-553A-46
7	217.2	56.7	363	2	US-08-477-553A-50
8	213.2	56.7	357	2	US-08-652-816A-20
9	209.8	55.8	357	1	US-08-360-125-3
10	209.8	55.8	357	2	US-08-450-578-3
11	209.8	55.8	357	2	US-09-017-628-3
12	209.8	55.8	357	2	US-09-014-880-3
13	209.8	55.8	357	4	US-08-450-363-3
14	209.2	55.6	354	2	US-08-652-816A-23
15	207.8	55.3	369	4	US-08-793-450-3
16	205.4	54.6	321	2	US-08-477-553A-47
17	198.2	52.7	372	2	US-08-477-553A-48
18	180.4	48.0	291	3	US-08-851-362D-13
19	173.2	46.1	297	3	US-09-042-353-151
20	173.2	46.1	297	4	US-08-758-417A-415
21	172.2	45.8	243	3	US-09-042-353-148
22	172.2	45.8	243	4	US-08-758-417A-412
23	171.6	45.6	285	3	US-09-042-353-150
24	171.6	45.6	285	4	US-08-758-417A-414
25	171.4	45.6	282	3	US-09-042-353-149
26	171.4	45.6	282	4	US-08-758-417A-413
27	164.8	43.8	288	3	US-08-851-362D-15

28 160.4 42.7 294 3 US-08-851-362D-3
29 159.6 42.4 291 3 US-08-851-362D-11
30 159.2 42.3 354 3 US-09-065-059-12
31 158.4 42.1 288 3 US-08-851-362D-7
32 157.2 41.8 288 3 US-08-767-128-17
33 153.2 40.7 291 3 US-08-851-362D-5
34 150.4 40.0 300 2 US-08-273-146-68
35 150.4 40.0 366 2 US-08-672-345C-87
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37 150.4 40.0 366 3 US-09-214-095D-101
38 150.4 40.0 366 3 US-09-214-095D-105
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43 145.4 38.7 360 5 PCT-US93-10555-19
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45 143.8 38.2 360 2 US-08-428-197-23

ALIGNMENTS

RESULT 1
US-08-360-125-9
; Sequence 9, Application US/08360125
; Patent No. 5767246
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Toshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 5767246ihiko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; TITLE OF INVENTION: Cell Membrane
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360.125
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8950
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 366 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

Sequence 3, Appli
Sequence 11, Appl
Sequence 12, Appl
Sequence 7, Appli
Sequence 17, Appl
Sequence 5, Appli
Sequence 88, Appl
Sequence 89, Appl
Sequence 101, App
Sequence 105, App
Sequence 9, Appli
Sequence 17, Appl
Sequence 14, Appl
Sequence 19, Appl
Sequence 21, Appl
Sequence 23, Appl

US-08-450-578-9

Sequence 9, Application US/08450578
Patent No. 5837845
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Yoshiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 5837845shiko ITO
APPLICANT: Kazuhiro NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody
SPECIFICALLY BINDING TO SURFACE ANTIGEN OF CANCER
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,578
FILING DATE: May 25, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIOR APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 366 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human antibody 1-3-1
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:

US-08-360-125-9

Query Match 63.2%; Score 237.8; DB 1; Length 366;
Best Local Similarity 81.6%; Pred. No. 1.6e-65;
Matches 301; Conservative 0; Mismatches 62; Indels 6; Gaps 2;

QY 11 CAGCTGACGCTGCGAGGAGTGGGGCCCGAGGAGTGGTGAAGCTTCGGAGACCTGTCCCTC 70
DB 1 CAGCTGACGCTGCGAGGAGTGGGGCCCGAGGAGTGGTGAAGCTTCGGAGACCTGTCCCTC 60
QY 71 ACTGCGCTGTCTGTGTGGCTCTGTCTGAGCAGTAGTA---ACTGTGACCTGATCCGC 127
DB 61 ACTGCGCTGTCTGTGTGGCTCTGTCTGAGCAGTAGTA---ACTGTGACCTGATCCGC 120
QY 128 CAGCCCCCAGGAGGAGGAGTGGAGTGGAGTATCTCTGTGTAGTGGGGCCACC 187
DB 121 CAGCCCCCAGGAGGAGGAGTGGAGTGGAGTATCTATATATA---GTGGAGGAGCACC 177
QY 188 AACTACAAACCGCTCCCTCAAGAGTCGAGTCACTATTTTCAAGACACAGTCCCAAGAACAG 247
DB 178 TACTACAAACCGCTCCCTCAAGAGTCGAGTCACTATTTTCAAGACACAGTCCCAAGAACAG 237
QY 248 TTCTCCCTGAACTGAACTGTGACCGCCGAGACAGCGCGTGTATTACTGTGCCAGA 307
DB 238 TTCTCCCTGAACTGAACTGTGACCGCCGAGACAGCGCGTGTATTACTGTGCCAGG 297
QY 308 GATTGGGCCCAATAGCTGGAACACAGTATAGGCTTTCTGGGGCCAGGAGTCTCTGTCAAC 367
DB 298 GGGAGCTACGGGGCTACTACTACGGTATGAGCTCTGGGGCCAGGAGTCTCTGTCAAC 357
QY 368 GTCTCTCA 376
DB 358 GTCTCTCA 366

US-08-450-578-9

Sequence 9, Application US/08450578
Patent No. 5837845
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Yoshiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 5837845shiko ITO
APPLICANT: Kazuhiro NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody
SPECIFICALLY BINDING TO SURFACE ANTIGEN OF CANCER
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,578
FILING DATE: May 25, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIOR APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 366 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human antibody 1-3-1
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:

US-08-360-125-9

Query Match 63.2%; Score 237.8; DB 1; Length 366;
Best Local Similarity 81.6%; Pred. No. 1.6e-65;
Matches 301; Conservative 0; Mismatches 62; Indels 6; Gaps 2;

QY 11 CAGCTGACGCTGCGAGGAGTGGGGCCCGAGGAGTGGTGAAGCTTCGGAGACCTGTCCCTC 70
DB 1 CAGCTGACGCTGCGAGGAGTGGGGCCCGAGGAGTGGTGAAGCTTCGGAGACCTGTCCCTC 60
QY 71 ACTGCGCTGTCTGTGTGGCTCTGTCTGAGCAGTAGTA---ACTGTGACCTGATCCGC 127
DB 61 ACTGCGCTGTCTGTGTGGCTCTGTCTGAGCAGTAGTA---ACTGTGACCTGATCCGC 120
QY 128 CAGCCCCCAGGAGGAGGAGTGGAGTGGAGTATCTCTGTGTAGTGGGGCCACC 187
DB 121 CAGCCCCCAGGAGGAGGAGTGGAGTGGAGTATCTATATATA---GTGGAGGAGCACC 177
QY 188 AACTACAAACCGCTCCCTCAAGAGTCGAGTCACTATTTTCAAGACACAGTCCCAAGAACAG 247
DB 178 TACTACAAACCGCTCCCTCAAGAGTCGAGTCACTATTTTCAAGACACAGTCCCAAGAACAG 237
QY 248 TTCTCCCTGAACTGAACTGTGACCGCCGAGACAGCGCGTGTATTACTGTGCCAGA 307
DB 238 TTCTCCCTGAACTGAACTGTGACCGCCGAGACAGCGCGTGTATTACTGTGCCAGG 297
QY 308 GATTGGGCCCAATAGCTGGAACACAGTATAGGCTTTCTGGGGCCAGGAGTCTCTGTCAAC 367
DB 298 GGGAGCTACGGGGCTACTACTACGGTATGAGCTCTGGGGCCAGGAGTCTCTGTCAAC 357
QY 368 GTCTCTCA 376
DB 358 GTCTCTCA 366

US-08-450-578-9

Sequence 9, Application US/08450578
Patent No. 5837845
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Yoshiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 5837845shiko ITO
APPLICANT: Kazuhiro NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody
SPECIFICALLY BINDING TO SURFACE ANTIGEN OF CANCER
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,578
FILING DATE: May 25, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIOR APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 366 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human antibody 1-3-1
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:

US-08-360-125-9

Query Match 63.2%; Score 237.8; DB 1; Length 366;
Best Local Similarity 81.6%; Pred. No. 1.6e-65;
Matches 301; Conservative 0; Mismatches 62; Indels 6; Gaps 2;

QY 11 CAGCTGACGCTGCGAGGAGTGGGGCCCGAGGAGTGGTGAAGCTTCGGAGACCTGTCCCTC 70
DB 1 CAGCTGACGCTGCGAGGAGTGGGGCCCGAGGAGTGGTGAAGCTTCGGAGACCTGTCCCTC 60
QY 71 ACTGCGCTGTCTGTGTGGCTCTGTCTGAGCAGTAGTA---ACTGTGACCTGATCCGC 127
DB 61 ACTGCGCTGTCTGTGTGGCTCTGTCTGAGCAGTAGTA---ACTGTGACCTGATCCGC 120
QY 128 CAGCCCCCAGGAGGAGGAGTGGAGTGGAGTATCTCTGTGTAGTGGGGCCACC 187
DB 121 CAGCCCCCAGGAGGAGGAGTGGAGTGGAGTATCTATATATA---GTGGAGGAGCACC 177
QY 188 AACTACAAACCGCTCCCTCAAGAGTCGAGTCACTATTTTCAAGACACAGTCCCAAGAACAG 247
DB 178 TACTACAAACCGCTCCCTCAAGAGTCGAGTCACTATTTTCAAGACACAGTCCCAAGAACAG 237
QY 248 TTCTCCCTGAACTGAACTGTGACCGCCGAGACAGCGCGTGTATTACTGTGCCAGA 307
DB 238 TTCTCCCTGAACTGAACTGTGACCGCCGAGACAGCGCGTGTATTACTGTGCCAGG 297
QY 308 GATTGGGCCCAATAGCTGGAACACAGTATAGGCTTTCTGGGGCCAGGAGTCTCTGTCAAC 367
DB 298 GGGAGCTACGGGGCTACTACTACGGTATGAGCTCTGGGGCCAGGAGTCTCTGTCAAC 357
QY 368 GTCTCT

RESULT 2

REFERENCE/DOCKET NUMBER:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 366 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cdna
ORIGINAL SOURCE:
CELL TYPE: Hybridoma producing human antibody 1-3-1
US-09-014-880-9

Query Match 63.2%; Score 237.8; DB 2; Length 366;
Best Local Similarity 81.6%; Pred. No. 1.6e-65;
Matches 301; Conservative 0; Mismatches 62; Indels 6; Gaps 2;

QY 11 CAGCTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTC 70
DB 1 CAGCTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTC 60
QY 71 ACCTGCGCTGTCTCTGTGGTCTGTGTCAGAGTAGTA---ACTGGTGCAGTGGATCCGC 127
DB 61 ACCTGCACTGTCTGTGGTGGTCCATCAGCAGTAGTAGTTACTACTCGGGGTGGATCCGC 120
QY 128 CAGCCCCCAGGAGGAGGAGTGGAGTGGATTGGACGTATCTCTGCTAGTGGTGGGCCACC 187
DB 121 CAGCCCCCAGGAGGAGGAGTGGAGTGGATTGGAGTATCTATTATA---GTGGAGGACC 177
QY 188 AACTACAAACCGTCCCTCAGAGTGGAGTGCATCATTTTCACAGACAGTCCAGAACAG 247
DB 178 TACTACAAACCGTCCCTCAGAGTGGAGTGCATCACCATATCCGTAGACAGTCCAGAACAG 237
QY 248 TTCTCCCTGAACCTGAACCTGTGCACCGCGGACACAGCGCGTATTACTGTGGCCAGA 307
DB 238 TTCTCCCTGAACCTGAACCTGTGCACCGCGGACACAGCGCGTATTACTGTGGCCAG 297
QY 308 GATTGGGCCCAATAGCTGGAGAACACGCTAGGCTTCGGGGCCAGGAGTCCGTGGTACC 367
DB 298 GGGAGCTACGGGGGCTACTACTACGGTATGAGACGTCTGGGGCCAGGAGGACCGGTACC 357
QY 368 GTCTCCTCA 376
DB 358 GTCTCCTCA 366

RESULT 5
US-08-450-363-9
Sequence 9, Application US/08450363
Patent No. 6436434
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Yoshiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 6436434hiko ITO
APPLICANT: Kazuhiro NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
TITLE OF INVENTION: Cell Membrane
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESS: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,363
FILING DATE: May 25, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 366 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cdna
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human antibody 1-3-1
CELL LINE:
ORGANISLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-450-363-9

Query Match 63.2%; Score 237.8; DB 4; Length 366;
Best Local Similarity 81.6%; Pred. No. 1.6e-65;
Matches 301; Conservative 0; Mismatches 62; Indels 6; Gaps 2;

QY 11 CAGCTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTC 70
DB 1 CAGCTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTC 60

Query Match	57.9%;	Score 217.6;	DB 2;	Length 372;
Best Local Similarity	86.8%;	Pred. No. 3.8e-59;		
Matches 264;	Conservative 0;	Mismatches 34;	Indels 6;	Gaps 2;
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DbB				
QY	61	ACCTGCACCTGTCTCTGTGGTCCGT---CAGTAGTTCCTACTGGAGCTGGATCCGGCAG	117	
DbB				
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QY	118	CCCCCAGGGAGGGACCGGAGTGGATTGGGTATATCTATTACA---GTGGGAGCACCAAC	174	
DbB				
QY	191	TACAAACCGTCCCTCAAGAGTCGAGTCATCATTTCCACAAGACACGTCCAAGAACACAGTTC	250	
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QY	175	TACAAACCCCTCCCTCAGGAGTCGAGTCACCATATCAGTAGACACGTCCTCAAGAACACAGTTC	234	
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QY	251	TCCCTGAACCTGAATCTGTGACCCCGCGGACACGGCCGTGTATTACTGTGCCAGAGAT	310	
DbB				
QY	235	TCCCTGAAGCTGGGCTCTGTGACCCGCTGGGACACGGCCGTGTATTACTGTGGAGAGTT	294	
DbB				
QY	311	TGGG	314	
DbB				
QY	295	TTGG	298	
DbB				

```

1
2
3
4
5
6
7
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MOLECULE TYPE: DNA (genomic)

US-08-477-553A-50

Query Match 57.7%; Score 217; DB 2; Length 363;
Best Local Similarity 79.9%; Pred. No. 5.8e-59;
Matches 295; Conservative 0; Mismatches 65; Indels 9; Gaps 3;

QY 11 CAGCTGCAGCTCAGAGTCGGGCGCCAGAGTGGTGAAGCCCTCGAGACCCCTGTCCTC 70
DB 1 CAGGTGCAGTACAGAGTGGGCGCCAGAGTGGTGAAGCCCTCGAGACCCCTGTCCTC 60

QY 71 ACTCGGCTGCTCTGTGGTCTCTGTCAGCTAGTAACTGTCAGACAGTCAAGACAGTTC 130
DB 61 ACTCGGCTGCTCTGTGGTCTCTGTCAGCTAGTAACTGTCAGACAGTTCAGACAGTTC 117

QY 131 CCCCAGGGAAGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 190
DB 118 CCCCAGGGAAGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 174

QY 191 TCAACCCGTCCTCAAGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 250
DB 175 TCAACCCGTCCTCAAGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 234

QY 251 TCCCTGAACTGAACTCTGTGACCGCGCGCGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 310
DB 235 TCCCTGAACTGAACTCTGTGACCGCGCGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 294

QY 311 TGGGCGCCAAATAGCTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 370
DB 295 TGGGCGCCAAATAGCTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 351

QY 371 TC 372
DB 352 TC 353

RESULT 9
US-08-652-816A-20
; Sequence 20, Application US/08652816A
; Patent No. 5872215
; GENERAL INFORMATION:
; APPLICANT: Osbourn, JK
; APPLICANT: Allen, DJ
; APPLICANT: McCafferty, JG
; TITLE OF INVENTION: Specific binding members, materials and methods.
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,816A
; FILING DATE: 23-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9125579.4
; FILING DATE: 02-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9125579.8
; FILING DATE: 02-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206372.6
; FILING DATE: 23-SEP-1992

CORRESPONDENCE ADDRESS:
ADDRESS: Wender-och, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,125
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:

FORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 357 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human
CELL TYPE: antibody GAK
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:

RESULT 10
 US-08-450-578-3
 ; Sequence 3, Application US/08450578
 ; Patent No. 5837845
 ; GENERAL INFORMATION:
 ; APPLICANT: Saiko HOSOKAWA
 ; APPLICANT: Toshiaki TAGAWA
 ; APPLICANT: Yoko HIRAKAWA
 ; APPLICANT: No. 5837845biko ITO
 ; APPLICANT: Kazuhiro NAGAIKE
 ; TITLE OF INVENTION: Human Monoclonal Antibody
 ; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
 ; TITLE OF INVENTION: Cell Membrane
 ; NUMBER OF SEQUENCES: 42
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Wenderoth, Lind & Ponack
 ; STREET: 805 Fifteenth Street, N.W., #700
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: MS-DOS
 ; SOFTWARE: WordPerfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/450,578
 ; FILING DATE: May 25, 1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/360,125
 ; FILING DATE: December 20, 1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/905,534
 ; FILING DATE: June 29, 1992
 ; ATTORNEY/AGENT INFORMATION:

```

1 NAME: Warren M. Cheek, Jr.
2 REGISTRATION NUMBER: 33,367
3 REFERENCE/DOCKET NUMBER:
4 TELECOMMUNICATION INFORMATION:
5 TELEPHONE: 202-371-8850
6 TELEFAX:
7 TELEX:
8 INFORMATION FOR SEQ ID NO: 3:
9 SEQUENCE CHARACTERISTICS:
10 LENGTH: 357 base pairs
11 TYPE: nucleic acid
12 STRANDEDNESS: double
13 TOPOLOGY: linear
14 MOLECULE TYPE: cDNA
15 HYPOTHETICAL:
16 ANTI-SENSE:
17 FRAGMENT TYPE:
18 ORIGINAL SOURCE:
19 ORGANISM:
20 STRAIN:
21 INDIVIDUAL ISOLATE:
22 DEVELOPMENTAL STAGE:
23 HAPLOTYPE:
24 TISSUE TYPE:
25 CELL TYPE: Hybridoma producing human
26 CELL TYPE: antibody GAH
27 ORGANELLE:
28 IMMEDIATE SOURCE:
29 LIBRARY:
30 CLONE:
31 POSITION IN GENOME:
32 CHROMOSOME/SEGMENT:
33 MAP POSITION:
34 UNITS:
35 FEATURE:
36 NAME/KEY:
37 LOCATION:
38 IDENTIFICATION METHOD:
39 OTHER INFORMATION:
40 PUBLICATION INFORMATION:
41 AUTHORS:
42 TITLE:
43 JOURNAL:
44 VOLUME:
45 ISSUE:
46 PAGES:
47 DATE:
48 DOCUMENT NUMBER:
49 FILING DATE:
50 PUBLICATION DATE:
51 RELEVANT RESIDUES IN SEQ ID NO:
52 US-08-450-578-3

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Query Match	55.8%;	Score 209.8;	DB 2;	Length 357;
Best Local Similarity	79.1%;	Pred. No. 1.1e-56;		
Matches	292;	Conservative 0;	Mismatches 62;	Indels 15; Gaps 3;
QY	11	CAGCTGCAGCTGCAGGAGTCGGGCCACAGGAGTGGTGAAGCCTTCGGAGACCTCTGTCCTC	70	
DB	1	CAGTGCAGCTGCAGGAGTCGGGCCACAGGAGTGGTGAAGCCTTCACAGACCTGTCCTC	60	
QY	71	ACTTGGCTCTCTCTGTGTGCTCTGTCAACA---GTAGTAACTGGTGGACCTGGAATCCGC	127	
DB	61	ACCTGCACTCTCTCTGTGTGCTCTCACTCAGCAGATTGTGGTTCCTACTGGAACCTGGAATCCGC	120	
QY	128	CAGCCCCACGGGAAGGACCTGGAGTGAATTGGACGTATCTCTGTAGTGGTGGGGCCACC	187	
DB	121	CAGCACCCACGGGAAGGSCCTGGAGTGGGTGATCTATTACA---GTGGGAGGACC	177	
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DB	178	TACTTACAACCCGTCCTCAAGAGTCGAGTACCAATATCGGTAGACAGCTCTAAGAGCCAG	237	

Qy	248	TTCTCCCTGAACCTGAACTCTCTGTGACCCGCCCGGACACAGCCCGCTGTATTACTGTGC	30
Db	238	TTCTCCCTGAACCTGAGCTCTCTGACTCCCGCGACACAGCCCGGTATTACTGTGCGAGG	297
Qy	308	GATTGGGGCCCCAAATAGCTGGGAACAACGCTTAGCGCTTCTGGGGGCCAGGGAGTCTCTGC	367
Db	298	TCTACCCGACTACGGG-----GGGCTGACTACTCTGGGGCCAGGGAAACAATGGTCACC	348
Qy	368	GTCTCTCTCA	376
Db	349	GATCTCTTCA	357

RESULT 11
 US-09-017-628-3
 ; Sequence 3, Application US/09017628
 ; Patent No. 5930287
 ; GENERAL INFORMATION:
 ; APPLICANT: HOSOKAWA, Saiko
 ; APPLICANT: TAGAWA, Toshiaki
 ; APPLICANT: HIRAKAWA, Yoko
 ; APPLICANT: ITO, No. 5990287ihiko
 ; APPLICANT: NAGAIKE, Kazuhiro
 ; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO
 ; TITLE OF INVENTION: SURFACE ANTIGEN OF CANCER CELL MEMBRANE
 ; FILE REFERENCE: 177/527361KH
 ; CURRENT APPLICATION NUMBER: US/09/017,628
 ; CURRENT FILING DATE: 1998-02-02
 ; EARLIER APPLICATION NUMBER: 08/360,125
 ; EARLIER FILING DATE: 1994-12-20
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 3
 ; LENGTH: 357
 ; TYPE: DNA
 ; ORGANISM: Unknown
 ; FEATURE:
 ; OTHER INFORMATION: Hybridoma producing human antibody G4H
 US-09-017-628-3

Query Match	55.8%;	Score	209.8;	DB 2;	Length	357;			
Best Local Similarity	79.1%;	Pred. No.	1.1e-56;						
Matches	292;	Conservative	0;	Mismatches	62;	Indels	15;	Gaps	3;
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Qy	11	CAGCTGCAGCTGCAGAGTCCGGCCACGAGTGGTGAAGCCTTCGAGACCCCTGTCCCTC	70						
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Qy	71	ACCTGGCGTGTCTCTGTGGCTCTGTCAACA---GTAGTAACTGGTGGACCTGGATCCGC	127						
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Qy	128	CAGCCCCCAGGAGGACCTGGAGTGGATTTGGACGTATCTCTGGTAGTGGTGGGCCACC	187						
Db	121	CAGACCCAGGAGGAGGCCCTGGAGTGGATTTGGGTACATCTATTACA---GTGGAGGACC	177						
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Db	178	TACTACAAACCGTCCCTCAAGAGTCGAGTTCACATATCGCTAGACACGCTAAGAGGCAG	237						
Qy	248	TTCTCCCTGAACCTGAACCTCTGTGACCGCCCGGACACCGCCGTGTATTACTGCGCAGA	307						
Db	238	TTCTCCCTGAAGCTGAGCTCTGTGATGCGCCGCGACACCGCCGTGTATTACTGTGCGAGG	297						
Qy	308	GATTGGGCCCAATAGCTGGAACAACGCTAGGCTTTCTGGGCGCCAGGAGTCTTGCTCACC	367						
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Db	349	GTCTCTTCA	357						

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Db 238 TTCTGTGAGCTGACTCTGTGACCGCCGCGGACACGCGCGTATTACTGTGTGCCAGATCT 297
Qy 311 TGGGCCCAAAATAGCTGGAAACAGCGTAGCTTCTGGGCGCCAGGGAGTCTCTGTGCACCGTC 370
Db 298 GAG-----CCTACCGCCCAACTTTGATTCTTGGGCGCAGGGGCAACCCCTGTGCACCGTC 348
Qy 371 TC 372
Db 349 TC 350

RESULT 15
US-08-793-450-3
; Sequence 3, Application US/08793450
; Patent No. 6312690
; GENERAL INFORMATION:
; APPLICANT: EDELMAN, LENA
; APPLICANT: MARGARITTE, CHRISTEL
; APPLICANT: KACZOREK, MICHEL
; APPLICANT: CHAABIHI, HASSAN
; TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793,450
; FILING DATE: 03-MAR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94/10566
; FILING DATE: 02-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN P.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 660-118-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 369 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..369
; OTHER INFORMATION: /product= "IMMUNOGLOBIN VARIABLE
; OTHER INFORMATION: REGION"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 91..105
; OTHER INFORMATION: /label= CDRI
; FEATURE:
; NAME/KEY: misc feature

; LOCATION: 148..195
; OTHER INFORMATION: /label= CDR2
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 292..336
; OTHER INFORMATION: /standard_name= "CDR3"
US-08-793-450-3
Query Match 55.3%; Score 207.8; DB 4; Length 369;
Best Local Similarity 78.1%; Pred. No. 4.6e-56;
Matches 293; Conservative 0; Mismatches 67; Indels 15; Gaps 3;
Qy 11 CAGCTGCAGCTGCAGGAGTCGSGCCCAAGGAGTGTGTAAGCTTCGGAGACCCCTGTCTCCCTC 70
Db 1 CAGGTCCAACTGCAGCAGTGGGGCGCAGGACTGTTGAAGCTTCGGAGACCCCTGTCTCCCTC 60
Qy 71 ACTTGGCTGTCTCTGTGTGCTCTGTTCAGCAGTAGTAACCTGGTGGACCTGGATCCGCGCAG 130
Db 61 ACTTGCACTGTCTATGGTGGCTC---CTTCAGTGGTTACTACTCTGAGCTGGATCCGCGCAG 117
Qy 131 CCCCCAGGGAAGGAGCTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGGCCCAACCAAC 190
Db 118 CCCCCAGGGAAGGGGCTGGAGTGGATTGGGGAATCAATCATAGTGAAG---CAACCAAC 174
Qy 191 TACAACCCGTCCTCAAGAGTCCAGAGTCATCATTTTCAAGACACAGCTCCAAGAACCAAGTTC 250
Db 175 TACAACCCGTCCTCAAGAGTCCAGAGTCACCATATCAGTAGACACGTCCTCAAGAACCAAGTTC 234
Qy 251 TCCCTGAACCTGAACCTCTGTGACCGCCGCGGACACGCGCGTGTATTACTGTGCCAGAGAT 310
Db 235 TCCCTGAACCTGAACCTCTGTGACCGCCGCGGACACGCGCTGTGTATTACTGTGGAGGGCC 294
Qy 311 TGGGCCCAAAATA-----GCTGGAAACAAACGCTAGGCTTCTGGGGCCCAAGGAGTCTG 361
Db 295 CCAGAGTATTAATGGAAGTATCATGGGACTGTGGTTCGACCCCTGGGGCCCAAGGTACCACT 354
Qy 362 GTCACCGTCTCCTCA 376
Db 355 GTCACCGTCTCCTCA 369
Search completed: June 19, 2004, 07:32:31
Job time : 64 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2004, 07:02:32 ; Search time 283 Seconds
(without alignments)
6086.536 Million cell updates/sec

Title: US-09-019-441A-3_COPY_48_423

Perfect score: 376
Sequence: 1 ggccgtccacgtcagc.....tctgttcacgtctctctca 376

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 2667516

Minimum DB seq length: 0

Maximum DB seq length: 376

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*

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- 2: /cgm2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgm2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 4: /cgm2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgm2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 6: /cgm2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgm2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 8: /cgm2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 9: /cgm2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgm2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgm2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgm2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 13: /cgm2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2.*
- 14: /cgm2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 15: /cgm2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 16: /cgm2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 17: /cgm2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 18: /cgm2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 19: /cgm2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	249.2	56.3	361	16	US-10-309-762-208
2	246	55.4	361	16	US-10-309-762-118
3	246	55.4	361	16	US-10-309-762-182
4	246	55.4	361	16	US-10-309-762-206
5	241.4	64.2	296	17	US-10-038-591-33
6	235.4	62.6	358	17	US-10-038-591-57
7	235.2	62.6	356	17	US-10-388-214A-35
8	235.2	62.6	356	17	US-10-388-214A-37
9	235.2	62.6	362	9	US-09-864-761-32297
10	234.8	62.4	367	16	US-10-309-762-183
11	234.8	62.4	367	16	US-10-309-762-196
12	234.6	62.4	364	13	US-10-292-088-97
13	233.8	62.2	319	9	US-09-864-761-28401
14	233.2	62.0	367	16	US-10-309-762-116

15	233.2	62.0	367	16	US-10-309-762-181
16	233	62.0	352	16	US-10-309-762-203
17	233	62.0	364	13	US-10-292-088-65
18	233	62.0	364	13	US-10-292-088-81
19	231.8	61.6	361	16	US-10-309-762-193
20	231.6	61.6	357	13	US-10-292-088-17
21	231.2	61.5	370	16	US-10-309-762-186
22	229.8	61.1	367	16	US-10-309-762-195
23	228.2	60.7	363	13	US-10-292-088-25
24	228.2	60.7	363	15	US-10-067-800-59
25	228	60.6	370	16	US-10-309-762-185
26	226.4	60.2	349	12	US-10-269-711-2
27	225.8	60.1	375	13	US-10-371-942-117
28	225.4	59.9	293	17	US-10-038-591-43
29	225.4	59.9	364	17	US-10-038-591-59
30	223.8	59.5	293	17	US-10-038-591-35
31	223.2	59.4	369	13	US-10-371-942-101
32	223.2	59.4	373	16	US-10-309-762-192
33	222.6	59.2	358	15	US-10-330-613-27
34	222.6	59.2	358	15	US-10-330-530-27
35	222.2	59.1	370	16	US-10-309-762-204
36	221.8	59.0	361	16	US-10-309-762-191
37	221.8	59.0	364	15	US-10-330-613-11
38	221.8	59.0	364	15	US-10-330-613-39
39	221.8	59.0	364	15	US-10-330-530-11
40	220.8	59.0	364	15	US-10-330-530-39
41	220.8	58.7	324	9	US-09-864-761-31244
42	220.4	58.6	367	16	US-10-309-762-198
43	220.4	58.6	367	16	US-10-309-762-210
44	220.2	58.6	352	15	US-10-330-613-15
45	220.2	58.6	352	15	US-10-330-530-15

ALIGNMENTS

RESULT 1
US-10-309-762-208
; Sequence 208, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Poltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 208
; LENGTH: 361
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-309-762-208

Query Match	66.3%;	Score	249.2;	DB	16;	Length	361;
Best Local Similarity	83.9%;	Pred. No.	6.6e-68;				
Matches	307;	Conservative	0;	Mismatches	53;	Indels	6;
Gaps	2;						
QY	11	CAGTCCAGCTGCTCTCTGTGGTGGCTCTGTGACAGTAGTAATCTGGAGTGGATCCGCCAG	70				
Db	1	CAGTCCAGCTGCTCTCTGTGGTGGCTCTGTGACAGTAGTAATCTGGAGTGGATCCGCCAG	60				
QY	71	ACCTGCGCTGTCTCTGTGGTGGCTCTGTGACAGTAGTAATCTGGAGTGGATCCGCCAG	130				
Db	61	ACCTGCGCTGTCTCTGTGGTGGCTCTGTGACAGTAGTAATCTGGAGTGGATCCGCCAG	117				
QY	131	CCCCCAGGGAAGGAGCTGGAGTGGATCTCTGTGGTGGATCTCTGTGGTGGGCGCCACCAAC	190				

Db 118 CCGCGCGGAGGAGCTGGAGTGGATTGGCGTATCT--ATACAGTGGGAGCACCAC 174
Qy 191 TACAACCCGTCCTCAAGAGTCAGTGCATCATTTCAAGACACAGCTCAAGAACAGTTC 250
Db 175 TACAACCCCTCCCTCAAGAGTCAGTGCATCATTTCAAGACACAGCTCAAGAACAGTTC 234
Qy 251 TCCTGAACTGAACTCTGTGACCGCGGACACCGCGCTGTATTTACTGTGCGAGAT 310
Db 235 TCCTGAACTGAGCTCTGTGACCGCGGACACCGCGCTGTATTTACTGTGCGAGAT 294
Qy 311 TGGGCCCCAATAGCTGGAACAACGCTAGGCTTCTGGGCGCAGGAGTCTGTGTCACCGTC 370
Db 295 CAGGAGTTTGGAGTGTTACTCTGAGAGCTCTGGGCGCAGGAGTCTGTGTCACCGTC 354
Qy 371 TCCTCA 376
Db 355 TCCTCA 360

RESULT 2
US-10-309-762-118
; Sequence 118, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 118
; LENGTH: 361
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-309-762-118

Query Match 65.4%; Score 246; DB 16; Length 361;
Best Local Similarity 83.3%; Pred. No. 6.6e-67;
Matches 305; Conservative 0; Mismatches 55; Indels 6; Gaps 2;

Qy 11 CAGCTGCAGCTGCAGGAGTCGGGCGCCAGGAGTGGTGAAGCTTCGGAGACCTGTCCCTC 70
Db 1 CAGGTGCAGCTGCAGGAGTCGGGCGCCAGGAGTGGTGAAGCTTCGGAGACCTGTCCCTC 60
Qy 71 ACCTGCGCTGTCTCTGTGGTGGCTCTGTGACAGTGTAACTGTGTGAGCTGGATCCGCGAG 130
Db 61 ACCTGCACTGTCTCTGTGGTGGCTC--CATCAGTAGTTACTTGTGAGCTGGATCCGCGAG 117
Qy 131 CCGCGAGGAGGAGGAGTGGAGTGGAGTTGAGCTATCTCTGTGTAGTGGGCGCCACCAAC 190
Db 118 CCGCGAGGAGGAGGAGTGGAGTGGAGTTGAGCTATCT--ATACAGTGGGAGCACCAC 174
Qy 191 TACAACCCGTCCTCAAGAGTCAGTGCATCATTTCAAGACACAGCTCAAGAACAGTTC 250
Db 175 TACAACCCCTCCCTCAAGAGTCAGTGCATCATTTCAAGACACAGCTCAAGAACAGTTC 234
Qy 251 TCCTGAACTGAACTCTGTGACCGCGGACACCGCGCTGTATTTACTGTGCGAGAT 310
Db 235 TCCTGAACTGAGCTCTGTGACCGCGGACACCGCGCTGTATTTACTGTGCGAGAT 294
Qy 311 TGGGCCCCAATAGCTGGAACAACGCTAGGCTTCTGGGCGCAGGAGTCTGTGTCACCGTC 370
Db 295 GCGGAGTGGCTGGAAGACTACGATGAGCTCTGGGCGCAGGAGTCTGTGTCACCGTC 354
Qy 371 TCCTCA 376

Db 355 TCCTCA 360

RESULT 3
US-10-309-762-182
; Sequence 182, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 182
; LENGTH: 361
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-309-762-182

Query Match 65.4%; Score 246; DB 16; Length 361;
Best Local Similarity 83.3%; Pred. No. 6.6e-67;
Matches 305; Conservative 0; Mismatches 55; Indels 6; Gaps 2;

Qy 11 CAGCTGCAGCTGCAGGAGTCGGGCGCCAGGAGTGGTGAAGCTTCGGAGACCTGTCCCTC 70
Db 1 CAGGTGCAGCTGCAGGAGTCGGGCGCCAGGAGTGGTGAAGCTTCGGAGACCTGTCCCTC 60
Qy 71 ACCTGCGCTGTCTCTGTGGTGGCTCTGTGACAGTGTAACTGTGTGAGCTGGATCCGCGAG 130
Db 61 ACCTGCACTGTCTCTGTGGTGGCTC--CATCAGTAGTTACTTGTGAGCTGGATCCGCGAG 117
Qy 131 CCGCGAGGAGGAGGAGTGGAGTGGAGTTGAGCTATCTCTGTGTAGTGGGCGCCACCAAC 190
Db 118 CCGCGAGGAGGAGGAGTGGAGTGGAGTTGAGCTATCT--ATACAGTGGGAGCACCAC 174
Qy 191 TACAACCCGTCCTCAAGAGTCAGTGCATCATTTCAAGACACAGCTCAAGAACAGTTC 250
Db 175 TACAACCCCTCCCTCAAGAGTCAGTGCATCATTTCAAGACACAGCTCAAGAACAGTTC 234
Qy 251 TCCTGAACTGAACTCTGTGACCGCGGACACCGCGCTGTATTTACTGTGCGAGAT 310
Db 235 TCCTGAACTGAGCTCTGTGACCGCGGACACCGCGCTGTATTTACTGTGCGAGAT 294
Qy 311 TGGGCCCCAATAGCTGGAACAACGCTAGGCTTCTGGGCGCAGGAGTCTGTGTCACCGTC 370
Db 295 GCGGAGTGGCTGGAAGACTACGATGAGCTCTGGGCGCAGGAGTCTGTGTCACCGTC 354
Qy 371 TCCTCA 376
Db 355 TCCTCA 360

RESULT 4
US-10-309-762-206
; Sequence 206, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A

;; PRIOR FILING DATE: 2001-12-03
;; NUMBER OF SEQ ID NOS: 246
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 196
;; LENGTH: 367
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-309-762-196

Query Match 62.4%; Score 234.8; DB 16; Length 367;
Best Local Similarity 82.8%; Pred. No. 2.1e-63;
Matches 308; Conservative 0; Mismatches 52; Indels 12; Gaps 3;

Qy 11 CAGCTGCAGCTGCAGGAGTCCGGGCCAGGAGTGGTGAAGCCCTCGGAGACCCCTGTCCCTC 70
Db 1 CAGGTGCAGCTGCAGGAGTCCGGGCCAGGAGTGGTGAAGCCCTCGGAGACCCCTGTCCCTC 60
Qy 71 ACCTGCGCTGCTCTGCTGGCTCTGTGAGCTAGTATCTTCAAGACAGTGGTGGTCCGCGCAG 130
Db 61 ACCTGCACTGCTCTGCTGGCTCTGTGAGCTAGTATCTTCAAGACAGTGGTGGTCCGCGCAG 117
Qy 131 CCCCAGGAGGAGGAGTGGAGTGGATGAGTATCTCTGCTAGTGGTGGGCGCCACCAAC 190
Db 118 CCCCAGGAGGAGGAGTGGAGTGGATGAGTATCTTATTA---GTGGGAGCACCAAC 174
Qy 191 TACACCCGCTCCCTCAGAGTGGAGTGCATCAATTTACACAGACAGTCCCAAGAACCAATTC 250
Db 175 TACACCCCTCCCTCAGAGTGGAGTGCATCAATTTACACAGACAGTCCCAAGAACCAATTC 234
Qy 251 TCCCTGAACCTGAACTCTGTGACCGCGCGGACACGCGCGTGTATTTACTGTGCCAGAGAT 310
Db 235 TCCCTGAAGCTGAACTCTGTGACCGCGCGGACACGCGCGTGTATTTACTGTGCCAGAGAT 294
Qy 311 TGGGCCCAATAGCTG---GACACAGCTAGAGTCTTGGGGCCAGGAGTCTTGGTCAAC 367
Db 295 GGGTACGATATTTGACTGTTGACTTATGACTTCTGACTTGGGGCCAGGAGTCTTGGTCAAC 354
Qy 365 ACCGCTCCTCA 376
Db 355 ACCGCTCCTCA 366

RESULT 12
US-10-292-088-97
; Sequence 97, Application US/10292088
; Publication No. US2003021100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PP/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 364
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-292-088-97

Query Match 62.4%; Score 234.6; DB 13; Length 364;
Best Local Similarity 82.9%; Pred. No. 2.4e-63;
Matches 306; Conservative 0; Mismatches 54; Indels 9; Gaps 3;

Qy 11 CAGCTGCAGCTGCAGGAGTCCGGGCCAGGAGTGGTGAAGCCCTCGGAGACCCCTGTCCCTC 70
Db 1 CAGGTGCAGCTGCAGGAGTCCGGGCCAGGAGTGGTGAAGCCCTCGGAGACCCCTGTCCCTC 60

Qy 71 ACCTGCGCTGCTCTGCTGGTCTGTGACAGTATTAAGTGGTGGACCTGGATCCGCCAG 130
Db 61 ACCTGCACTGCTCTGCTGGTCTGTGACAGTATTAAGTGGTGGACCTGGATCCGCCAG 117
Qy 131 CCCCAGGAGGAGGAGTGGAGTGGATGAGTATCTCTGCTAGTGGTGGGCGCCACCAAC 190
Db 118 CCCCCTGGGAGGAGTGGAGTGGATGAGTATCTTATTA---GTGGGAGCACCAAC 174
Qy 191 TACACCCGCTCCCTCAGAGTGGAGTGCATCAATTTACACAGACAGTCCCAAGAACCAATTC 250
Db 175 TACACCCCTCCCTCAGAGTGGAGTGCATCAATTTACACAGACAGTCCCAAGAACCAATTC 234
Qy 251 TCCCTGAACCTGAACTCTGTGACCGCGCGGACACGCGCGTGTATTTACTGTGCCAGAGAT 310
Db 235 TCCCTGAAGCTGAACTCTGTGACCGCGCGGACACGCGCGTGTATTTACTGTGCCAGAGAT 294
Qy 311 TGGGCCCAATAGCTG---GACACAGCTAGAGTCTTGGGGCCAGGAGTCTTGGTCAAC 367
Db 295 GGGTACGATATTTGACTGTTGACTTATGACTTCTGACTTGGGGCCAGGAGTCTTGGTCAAC 354
Qy 368 GTCTCCTCA 376
Db 355 GTCTCCTCA 363

RESULT 13
US-09-864-761-28401
; Sequence 28401, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn. Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aemica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408

[illegible]

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RESULT 15
US-10-309-762-181
? Sequence 181, Application US/10309762
? Publication No. US20040018198A1
? GENERAL INFORMATION:
? APPLICANT: Gudas, Jean
? APPLICANT: Foltz, Ian
? APPLICANT: Hands, Masahisa
? APPLICANT: Gallo, Michael
? TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYC ANHYDRASE IX
? TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
? FILE REFERENCE: ABGENIX.027A
? CURRENT APPLICATION NUMBER: US/10/309,762
? CURRENT FILING DATE: 2002-12-02
? PRIOR APPLICATION NUMBER: 60/337275
? PRIOR FILING DATE: 2001-12-03
? NUMBER OF SEQ ID NOS: 246
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 181
? LENGTH: 367
? TYPE: DNA
? ORGANISM: Homo sapiens
US-10-309-762-181

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	Query Match	62.0%;	Score 233.2;	DB 16;	Length 367;
	Best Local Similarity	82.5%;	Pred. No. 6.7e-63;		
	Matches 307;	Conservative 0;	Mismatches 53;	Indels 12;	Gaps 3;
QY	11	CAGCTGCACCTCGCAGAGTCGGGCCCCAGAGTAGTGTCGAAGCCTTCGAGAGACCCCTGTCTCCCTC	70		
DB	1	CAGCTGCACCTCGCAGAGTCGGGCCCCAGACTGCTGAAGCCCTTCGAGAGACCCCTGTCTCCCTC	60		
QY	71	ACCTGGCTGTCTCTGGTGGCTCTGTTCAGCAGTAGTAACCTGGTGGACCTGGATCCGGCAG	130		
DB	61	ACCTGCACCTGTCTCTGGTGGCTC---CATCAGTAGTTACTACTCGAGCTGGATCCGGCAG	117		
QY	131	CCCCCAGGGAAGGGACTCGAGTGGATTGGACGCTATCTCTGGTAGTCGGTGGGGCCACCAC	190		
DB	118	CCCCCAGGGAAGGACTCGAGTGGATTGGGTATATCTATTACA---GTGGGAGCACCAC	174		
QY	191	TACAACCCCTCCCTCAAGAGTCGAGTCATCATTTTCACAAGACACGCTCCAAAGACCGAGTTC	250		
DB	175	TACAACCCCTCCCTCAAGAGTCGAGTCACCATATCATGTAGACACGCTCCAAAGACCGAGTTC	234		

Qy	251	TCCCTGAACCTGA	310
Db	235	TCCCTGAACCTGA	294
Qy	311	TGGGCCCA-----AATAGCTGGAACACGCTAGGCTTCTGGGCCCAAGGAGTCTGGTC	364
Db	295	GGGTACGACTTTTGGACTGGTTATGACTACTTTGACTACTGGGGCCAGGGAACCTGGTC	354
Qy	365	ACCGTCTCCTCA	376
Db	355	ACCGTCTCCTCA	366

Search completed: June 19, 2004, 08:16:39
Job time : 285 secs

OM nucleic - nucleic search, using sw model

Run on: June 19, 2004, 06:19:02 ; Search time 1733 Seconds
(without alignments)
6479.042 Million cell updates/sec

Title: US-09-019-441A-3_COPY_48_423
Perfect score: 376
Sequence: 1 ggtctgcccagctgcagc.....tcctgggtcacgcgtctctcca 376

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 13781830

Minimum DB seq length: 0
Maximum DB seq length: 376

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_hcc:*
- 9: gb_est1:*
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- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: em_gss_hum:*
- 18: em_gss_inv:*
- 19: em_gss_pln:*
- 20: em_gss_vrt:*
- 21: em_gss_fun:*
- 22: em_gss_mam:*
- 23: em_gss_mus:*
- 24: em_gss_pro:*
- 25: em_gss_rpd:*
- 26: em_gss_pbg:*
- 27: em_gss_vrl:*
- 28: gb_gss1:*
- 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	228.4	60.7	374	10 AW403845	AW403845 UI-HF-BKO
2	224.6	59.7	319	10 AW405472	AW405472 UI-HF-BKO
3	218.8	58.2	369	10 AW404242	AW404242 UI-HF-BKO
4	217.8	57.9	370	10 AW402748	AW402748 UI-HF-BKO

5	217	57.7	367	10	AW403544	AW403544 UI-HF-BKO
6	216.8	57.7	353	10	AW401636	AW401636 UI-HF-BKO
7	215.2	57.2	363	10	AW403420	AW403420 UI-HF-BKO
8	212.8	56.6	368	10	AW403989	AW403989 UI-HF-BKO
9	208.6	55.5	358	12	BM820975	BM820975 K-EST0089
10	208.4	55.4	374	10	AW732986	AW732986 bbl8e10.Y
11	207.6	55.2	365	12	BI225611	BI225611 602948938
12	207.2	55.1	340	10	AW503526	AW503526 UI-HF-BKO
13	207	55.1	361	10	BF767440	BF767440 CMI-CN006
14	206.6	54.9	347	14	CD704336	CD704336 EST20863
15	204.8	54.5	342	10	AW733058	AW733058 bbl20e05.Y
16	204.2	54.3	345	10	BE167630	BE167630 CMO-HT050
17	204.2	54.3	357	12	BP432480	BP432480 BP432480
18	202.2	53.8	310	10	AW401919	AW401919 UI-HF-BKO
19	198.2	52.7	347	10	BF871155	BF871155 MRL-ET014
20	189.4	50.4	275	10	AW408669	AW408669 UI-HF-BKO
21	183.8	48.9	347	10	BF871157	BF871157 MRL-ET014
22	183.2	48.7	354	10	BE932781	BE932781 CMI-HT086
23	177.4	47.2	273	10	BF847860	BF847860 IL5-ENO08
24	177.4	47.2	360	12	BM851875	BM851875 K-EST0132
25	175.6	46.7	368	10	AW842075	AW842075 RCO-CN002
26	175.4	46.6	270	10	BF869898	BF869898 MRL-ET014
27	173.6	46.2	342	12	BM851855	BM851855 K-EST0132
28	172.2	45.8	360	10	BF173443	BF173443 MYE1430a
29	171	45.5	246	12	BI059470	BI059470 PM4-UT010
30	171	45.5	246	12	BI061844	BI061844 PM4-UT010
31	170.6	45.4	345	14	CD695048	CD695048 EST11571
32	169.2	45.0	258	9	AA360195	AA360195 EST69374
33	169	44.9	279	10	AW403538	AW403538 UI-HF-BKO
34	168.8	44.9	240	12	EG950423	EG950423 CM3-CT060
35	168.8	44.9	327	10	AW361882	AW361882 PM3-CT026
36	168.4	44.8	337	10	AW869764	AW869764 MRL-SN007
37	168	44.7	248	10	AW403144	AW403144 UI-HF-BKO
38	168	44.7	364	14	CD709855	CD709855 EST26382
39	166.6	44.3	306	10	BF174894	BF174894 MYE4006.M
40	165.6	44.0	331	14	T27715	T27715 EST13381.Hu
41	165	43.9	321	12	BI225601	BI225601 602948921
42	164.6	43.8	368	10	BF759686	BF759686 CMI-CT060
43	162	43.1	337	10	BF869893	BF869893 MRL-ET014
44	161.4	42.9	356	10	AW403007	AW403007 UI-HF-BKO
45	159	42.3	287	12	BG999993	BG999993 MR3-HN006

ALIGNMENTS

RESULT 1
AW403845
LOCUS
DEFINITION UI-HF-BKO-abl-h-02-0-UI.r1 NIH_MGC_36 Homo sapiens cdna clone
IMAGE:3056859 5', mRNA sequence.
ACCESSION AW403845
VERSION AW403845.1 GI:6922998
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 374)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Rco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cdNA Library Preparation: M.B. Soares Lab
cdNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

Seq primer: M13 Forward.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3061658"
 /tissue_type="lymph"
 /cell_type="germinal center B cells"
 /cell_line="MGC85"
 /lab_host="DH10B (LTI)"
 /clone_lib="NIH MGC 37"
 /note="Vector: p773-Pac; Site 1: NotI; Site 2: Eco RI;
 Constructed from size fractionated cytoplasmic mRNA
 (0.5-1.5kb). Directionally cloned. Cells provided by Louis
 M. Staudt, Ph.D. Library preparation by Maria de Fatima
 Bernaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Query Match 59.7%; Score 224.6; DB 10; Length 319;
 Best Local Similarity 88.4%; Pred. No. 5.5e-48;
 Matches 268; Conservative 0; Mismatches 29; Indels 6; Gaps 2;

QY 7 GTCCAGCTGCAGCTGCAGAGTCGGGCCCGAGAGTGGTGAAGCCCTCGGAGACCTGTC 66
 DB 6 GGGCCAGGTGCAGCTGCAGAGTCGGGCCCGAGAGTGGTGAAGCCCTCGGAGACCTGTC 65
 QY 67 CTTCCCTGCGTCTCTGTTGGCTCTGTGCAGCAGTGTAACTGTGACCTGGATCCG 126
 DB 66 CTTCCCTGCGTCTCTGTTGGCTCTGTGCAGCAGTGTAACTGTGACCTGGATCCG 122
 QY 127 CCAGCCCCCAGGAGGAGCTGGAGTGGATTCAGTATCTCTGTTAGTGGTGGGCCAC 186
 DB 123 GCAGCCCCCAGGAGGAGCTGGAGTGGATTCAGTATCTCTGTTAGTGGTGGGCCAC 179
 QY 187 CAATACACCGTCTCTGAGTGGATTCAGTATCTCTGTTAGTGGTGGGCCAC 246
 DB 180 CAATACACCGTCTCTGAGTGGATTCAGTATCTCTGTTAGTGGTGGGCCAC 239
 QY 247 GTTCTCCCTGAACTCTGTGACCGCCGAGAGTGGTGGTGGTGGGCCAG 306
 DB 240 GTTCTCCCTGAACTCTGTGACCGCCGAGAGTGGTGGTGGTGGGCCAG 299
 QY 307 AGA 309
 DB 300 ACA 302

RESULT 3
 AW404242
 LOCUS
 DEFINITION
 UI-HF-BLO-abq-f-09-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
 IMAGE:3057545 5', mRNA sequence.
 ACCESSION
 AW404242
 VERSION
 AW404242.1 GI:6923299
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 (bases 1 to 369)
 AUTHORS
 NIH-MGC http://mgi.nci.nih.gov/
 TITLE
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL
 Unpublished (1999)
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Eco RI site shown at the beginning of the sequence.
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: M.B. Soares Lab
 cDNA Library Arrayed by: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:

FEATURES
 source
 Location/Qualifiers
 1. .374
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3056859"
 /tissue_type="lymph"
 /cell_type="germinal center B cells"
 /cell_line="MGC85"
 /lab_host="DH10B (LTI)"
 /clone_lib="NIH MGC 36"
 /note="Vector: p773-Pac; Site 1: NotI; Site 2: Eco RI;
 Constructed from size fractionated cytoplasmic mRNA
 (0.5-1.5kb). Directionally cloned. Cells provided by Louis
 M. Staudt, Ph.D. Library preparation by Maria de Fatima
 Bernaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Query Match 60.7%; Score 228.4; DB 10; Length 374;
 Best Local Similarity 86.8%; Pred. No. 6.1e-49;
 Matches 276; Conservative 0; Mismatches 36; Indels 6; Gaps 2;

QY 1 GGTCTGCTCCAGCTGCAGCTGCAGAGTGGGCCCGAGAGTGGTGAAGCCCTCGGAGAC 60
 DB 26 GGTCTGCTCCAGCTGCAGCTGCAGAGTGGGCCCGAGAGTGGTGAAGCCCTCGGAGAC 85
 QY 61 CTTGCTCTACCTGCGTCTCTGTTGGCTCTGTGCAGCAGTGTAACTGTGACCTGGATCCG 117
 DB 96 CTTGCTCTACCTGCGTCTCTGTTGGCTCTGTGCAGCAGTGTAACTGTGACCTGGATCCG 145
 QY 118 CTGATCCCGCAGCCCCCAGGAGGAGTGGAGTGGATTCAGTATCTCTGTTAGTGG 177
 DB 146 CTGATCCCGCAGCCCCCAGGAGGAGTGGAGTGGATTCAGTATCTCTGTTAGTGG 202
 QY 178 TGGGCCCAACCACTACACCCGCTCTCAAGTGGATTCAGTATCTCTGTTAGTGG 237
 DB 203 TGGGAACACCTACTATATACCCGCTCTCAAGTGGATTCAGTATCTCTGTTAGTGG 262
 QY 238 CAAGAACCACTCTCTCTGAGCTGAGTCTGTGACCGCCGAGAGTGGTGGTGGTGGTATTA 297
 DB 263 CAAGAACCACTCTCTCTGAGCTGAGTCTGTGACCGCCAGAGTGGTGGTGGTGGTATTA 322
 QY 298 CTGTCGCCAGAGTGGGC 315
 DB 323 CTGTCGCCAGAGTGGGC 340

RESULT 2
 AW405472
 LOCUS
 DEFINITION
 UI-HF-BLO-adh-d-02-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
 IMAGE:3061658 5', mRNA sequence.
 ACCESSION
 AW405472
 VERSION
 AW405472.1 GI:6924529
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 (bases 1 to 319)
 AUTHORS
 NIH-MGC http://mgi.nci.nih.gov/
 TITLE
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL
 Unpublished (1999)
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Eco RI site shown at the beginning of the sequence.
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: M.B. Soares Lab
 cDNA Library Arrayed by: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html

www-bio.llnl.gov/bbrp/image/image.html

Seq primer: M13 Forward

FEATURES

source
Location/Qualifiers
1..369
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3057545"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/clone_lib="NIH_MGC_37"
/note="Vector: pVT3-Pac; Site 1: NotI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldio, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Query Match 58.2%; Score 218.8; DB 10; Length 369;
Best Local Similarity 84.9%; Pred. No. 1.9e-46;
Matches 270; Conservative 0; Mismatches 42; Indels 6; Gaps 2;
QY 1 GGTCTGTCCTCCAGCTGACAGTCCAGAGTCCGGCCAGAGTGGTGAAGCCCTTCGAGAC 60
DB 9 GGTCTGTCCTCCAGCTGACAGTCCAGAGTCCGGCCAGAGTGGTGAAGCCCTTCACAGAC 68
QY 61 CTTGTCCTCCAGCTGACAGTCCAGAGTCCGGCCAGAGTGGTGAAGCCCTTCGAGAC 117
DB 69 CTTGTCCTCCAGCTGACAGTCCAGAGTCCGGCCAGAGTGGTGAAGCCCTTCGAGAC 128
QY 118 CTGGATCCGCCAGCCCGCCAGGAGGACTGAGTGGATGGAAGTATCTCTGGTAGTGG 177
DB 129 CTGGATCCGCCAGCCCGCCAGGAGGACTGAGTGGATGGAAGTATCTCTGGTAGTGG 185
QY 178 TGGGCGCCAGCTACTACACCTCCCTCAAGAGTGGAGTCATCTTCAAGAGACACGTC 237
DB 186 TGGGCGCCAGCTACTACACCTCCCTCAAGAGTGGAGTCATCTTCAAGAGACACGTC 245
QY 238 CAAGAACCAAGTCTCTCCCTGAACTGAACTCTGTGACCGCCCGGACACGGCGGTATTA 297
DB 246 TAAGAACCAAGTCTCTCCCTGAACTGAACTCTGTGACCGCCCGGACACGGCGGTATTA 305
QY 298 CTGTGCCAGAGATTGGCC 315
DB 306 CTGTGCCAGAGATTGGCC 323

RESULT 4

AW402748
LOCUS
DEFINITION
UI-HF-BK0-aak-d-08-0-UI-ri NIH_MGC_36 Homo sapiens cDNA clone
IMAGE:3054014 5', mRNA sequence.

AW402748
VERSION
KEYWORDS
SOURCE
Homo sapiens (human)

AW402748.1 GI:6921476

AW402748.1 GI:6921476

AW402748.1 GI:6921476

AW402748.1 GI:6921476

AW402748.1 GI:6921476

AW402748.1 GI:6921476

AW402748.1 GI:6921476

AW402748.1 GI:6921476

AW402748.1 GI:6921476

AW402748.1 GI:6921476

AW402748.1 GI:6921476

AW402748.1 GI:6921476

AW402748.1 GI:6921476

AW402748.1 GI:6921476

AW402748.1 GI:6921476

AW402748.1 GI:6921476

AW402748.1 GI:6921476

AW402748.1 GI:6921476

AW402748.1 GI:6921476

AW402748.1 GI:6921476

AW402748.1 GI:6921476

AW402748.1 GI:6921476

AW402748.1 GI:6921476

AW402748.1 GI:6921476

AW402748.1 GI:6921476

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Seq primer: M13 Forward

FEATURES

source
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3054014"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/clone_lib="NIH_MGC_36"
/note="Vector: pVT3-Pac; Site 1: NotI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldio, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Query Match 57.9%; Score 217.8; DB 10; Length 370;
Best Local Similarity 86.1%; Pred. No. 3.5e-46;
Matches 266; Conservative 0; Mismatches 37; Indels 6; Gaps 2;
QY 1 GGTCTGTCCTCCAGCTGACAGTCCAGAGTCCGGCCAGAGTGGTGAAGCCCTTCGAGAC 60
DB 42 GGTCTGTCCTCCAGCTGACAGTCCAGAGTCCGGCCAGAGTGGTGAAGCCCTTCGAGAC 101
QY 61 CTTGTCCTCCAGCTGACAGTCCAGAGTCCGGCCAGAGTGGTGAAGCCCTTCGAGAC 120
DB 102 CTTGTCCTCCAGCTGACAGTCCAGAGTCCGGCCAGAGTGGTGAAGCCCTTCGAGAC 158
QY 121 GATCGCGCCAGCCCGCCAGGAGGACTGAGTGGATGGAAGTATCTCTGGTAGTGG 180
DB 159 GATCGCGCGCCAGCCCGCCAGGAGGACTGAGTGGATGGAAGTATCTCTGGTAGTGG 215
QY 181 GGCACCAACTACAACTCCCTCAAGAGTGGAGTCATCTTCAAGAGACACGTC 240
DB 216 GAGCATCAACTCCAACTCCCTCAAGAGTGGAGTCATCTTCAAGAGACACGTC 275
QY 241 GAACAGTCTTCCCTGAACTGAACTCTGTGACCGCCCGGACACGGCGGTATTA 300
DB 276 GAACAGTCTTCCCTGAACTGAACTCTGTGACCGCCCGGACACGGCGGTATTA 335
QY 301 TGCCAGAGA 309
DB 336 TGCCAGAGA 344

RESULT 5

AW403544

LOCUS

DEFINITION

UI-HF-BK0-abf-d-09-0-UI-ri NIH_MGC_36 Homo sapiens cDNA clone

IMAGE:3055937 5', mRNA sequence.

AW403544

VERSION

KEYWORDS

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 367)

NIH-MGC http://mgs.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

CONTACT: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: M.B. Soares Lab

cDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

cDNA Library Arrayed by: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab
 Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: M13 Forward

Location/Qualifiers
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 /tissue_type="lymph"
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 /clone_lib="NIH MGC 36"
 /notes="Vector: pT7T3-Pac; Site 1: NotI; Site 2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (0.5-1.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Query Match 57.2%; Score 215.2; DB 10; Length 363;
 Best Local Similarity 85.4%; Pred. No. 1.7e-45;
 Matches 264; Conservative 0; Mismatches 39; Indels 6; Gaps 2;

QY 1 GGTCTGTCCAGCTGCAGCTGCAGAGTGGGCCAGAGTGGTGAAGCTTCGAGAC 60
 Db 9 GGTCTGTCCAGCTGCAGCTGCAGAGTGGGCCAGAGTGGTGAAGCTTCAGAC 68
 QY 61 CCTGTCCCTCACCTGCCTCTCTCTGTGGTCTCTGTCTGAGCA---GTAGTAAGTGGTGGAC 117
 Db 69 CCTGTCCCTCACCTGCCTCTCTCTGTGGTCTCTGTCTGAGCAAGTGGTGTACTACTGGAC 128
 QY 118 CTGATCGCGCAGCTTCAGAGGAGGACCTGAGTGGATGGAGTATCTCTGGTAGTGG 177
 Db 129 CTGATCGCGCAGCTTCAGAGGAGGAGGAGTGGATGGAGTATCTCTGGTAGTGG 185
 QY 178 TGGGGCCACCACTACAGCCGCTCCCTCAAGAGTGGATGATCATATTTTCAGACACGCTC 237
 Db 186 TGGAGGGCTACTACATCCGCTCCCTCAAGAGTGGATGATCATATTTTCAGACACGCTC 245
 QY 238 CAAGAACCACTTCCTCTGACCTGAACTCTGTGACCGCGGACACGCGCGTGTATTA 297
 Db 246 TAAGAACCACTTCCTCTGACCTGAACTCTGTGACCTGCGGACACGCGCGTGTATTA 305
 QY 298 CTGTGCCAG 306
 Db 306 CTGTGTGAG 314

RESULT 8

AW403989
 LOCUS
 DEFINITION UI-HF-BK0-abl-d-08-0-UI-ri NIH MGC_36 Homo sapiens cDNA clone
 IMAGE:3056679 5', mRNA sequence.
 AW403989
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 368)
 NIH-MGC <http://imgc.nci.nih.gov/>
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Eco RI site shown at the beginning of the sequence.
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: M.B. Soares Lab
 cDNA Library Arrayed by: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab
 Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: M13 Forward

Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
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 /clone="IMAGE:3056679"
 /tissue_type="lymph"
 /cell_type="germinal center B cells"
 /cell_line="MGC85"
 /lab_host="DH10B (LTI)"
 /clone_lib="NIH MGC 36"
 /notes="Vector: pT7T3-Pac; Site 1: NotI; Site 2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (0.5-1.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Query Match 56.6%; Score 212.8; DB 10; Length 368;
 Best Local Similarity 84.6%; Pred. No. 7.1e-45;
 Matches 264; Conservative 0; Mismatches 42; Indels 6; Gaps 2;

QY 1 GGTCTGTCCAGCTGCAGCTGCAGAGTGGGCCAGAGTGGTGAAGCTTCGAGAC 60
 Db 42 GGTCTGTCCAGCTGCAGCTGCAGAGTGGGCCAGAGTGGTGAAGCTTCAGAC 101
 QY 61 CCTGTCCCTCACCTGCCTCTCTCTGTGGTCTCTGTCTGAGCAAGTGGTGTACTACTGGAC 117
 Db 102 CCTGTCCCTCACCTGCCTCTCTCTGTGGTCTCTGTCTGAGCAAGTGGTGTACTACTGGAC 161
 QY 118 CTGATCGCGCAGCTTCAGAGGAGGACCTGAGTGGATGGAGTATCTCTGGTAGTGG 177
 Db 162 CTGATCGCGCAGCTTCAGAGGAGGAGGAGTGGATGGAGTATCTCTGGTAGTGG 218
 QY 178 TGGGGCCACCACTACAGCCGCTCCCTCAAGAGTGGATGATCATATTTTCAGACACGCTC 237
 Db 219 TGGAGGGCTACTACATCCGCTCCCTCAAGAGTGGATGATCATATTTTCAGTAGACATGTC 278
 QY 238 CAAGAACCACTTCCTCTGACCTGAACTCTGTGACCGCGGACACGCGCGTGTATTA 297
 Db 279 TAAGAACCACTTCCTCTGACCTGAACTCTGTGACCTGCGGACACGCGCGTGTATTA 338
 QY 298 CTGTGCCAGAGA 309
 Db 339 CTGTGCCAGAGA 350

RESULT 9

BM820975
 LOCUS
 DEFINITION X-EST0089670 S19N665307 Homo sapiens cDNA clone S19N665307-9-C09
 5', mRNA sequence.
 BM820975
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 358)
 Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
 21C Frontier Korean EST Project 2001
 JOURNAL
 COMMENT Unpublished (2002)
 Contact: Kim YS

Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4470
Email: yongsung@mail.kribb.re.kr
Plate: 9 row: C column: 09
High quality sequence stop: 358.
Location/Qualifiers
1..358

FEATURES

source

/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="S19N65307-9-C09"
/sex="M"
/lab_host="Top10F"
/clone_lib="S19N65307"

/note="Organ: Stomach; Vector: pcNS; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 55.5%; Score 208.6; DB 12; Length 358;
Best Local Similarity 83.9%; Pred. No. 8.7e-44;
Matches 261; Conservative 0; Mismatches 44; Indels 6; Gaps 2;

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QY 1 GGTCTCTCCAGCTGCAGAGTGGGCCAGGAGTGTGAAGCTTCGGAGAC 60
Db 33 GGTCTCTCCAGTGCAGAGTGGGCCAGGAGTGTGAAGCTTCGGAGAC 92
QY 61 CTTGTCCCTCACCTGCGCTGTCTCTGTGGCTCTGTGACGAG---TAGTAACCTGGTGGAC 117
Db 93 CTTGTCCCTCACCTGCGCTGTCTCTGTGGCTCTGTGACGAGTCTTACTACTGGAG 152
QY 118 CTGATCCGCGAGCCCGCCAGGAGGAGTGGAGTGGATGGACGTATCTCTGGTAGTGG 177
Db 153 CTGGTCCGCGAGTCCCGCGGAGGAGCTGGAGTGGATGGAGCGGTATCT---ATACCTA 209
QY 178 TGGGGCCACCACTACAACCCGTCCTCAAGAGTCGAGTCATCATTTCAAGACACGTC 237
Db 210 TGGGAGCATCAACTACAATACCTCCCTCAAGATCGAGTCACCATATCAATAGACCCGTC 269
QY 238 CAGAGACCACTCTCCCTGACCTGACCTGTGACCGCGCGGAGACACGCGCTGTATTA 297
Db 270 CAGAGATCACTCTCCCTGAAGTGAACCTCTGTGACCGCGCGGAGACACGCGCTTATTA 329
QY 298 CTCTGCCAGAG 308
Db 330 CTGTGCTCGAG 340
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RESULT 10

AW732986

LOCUS

DEFINITION
bb18e10.y1 NIH MGC 8 Homo sapiens cDNA clone IMAGE:2963274 5'
similar to gb:M54911.rnal IG HEAVY CHAIN PRECURSOR V-II REGION
(HUMAN); mRNA sequence.

ACCESSION

AW732986

VERSION

AW732986.1 GI:76333328

KEYWORDS

EST.

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1. (bases 1 to 374)

NIH-MGC <http://mgc.nci.nih.gov/>.

AUTHORS

National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE

Unpublished (1999)

JOURNAL

Contact: Robert Strausberg, Ph.D.

COMMENT

Email: gsabbs@mail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: Ling Hong/Rubin Laboratory

DNA Sequencing by: The I.M.A.G.E. Consortium (LILNL)

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LILNL at:

image.lilnl.gov/image/html/iresources.shtml

Seq primer: -40RP from Glibco

High quality sequence stop: 334.

FEATURES

source

1..374

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2963274"

/tissue_type="Burkitt lymphoma"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH MGC 8"

/note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:

EcoRI; cDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCACGAG(G). Size-selected >500bp for average

insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 55.4%; Score 208.4; DB 10; Length 374;
Best Local Similarity 84.6%; Pred. No. 1e-43;
Matches 259; Conservative 0; Mismatches 41; Indels 6; Gaps 2;

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QY 1 GGTCTGTCCAGCTGCAGAGTGCAGAGTCCGGCCAGAGTGGTGAAGCTTCGGAGAC 60
Db 75 GGTCTGTCCAGTGCAGAGTGCAGAGTGGGGCGCAGAGCTGTTGAAGCTTCGGAGAC 134
QY 61 CTTGTCCCTCACCTGCGCTGTCTCTGTGGCTCTGTGACGAGTACTGTTGGACCTG 120
Db 135 CTTGTCCCTCACCTGCGCTGTCTCTGTGGCTCTGTGACGAGTACTGTTGGACCTG 191
QY 121 GATCCGCGCAGCCCGCCAGGAGGAGGACTGGAGTGGATGGAGCTATCTCTGGTAGTGG 180
Db 192 GATCCGCGCAGCCCGCCAGGAGGAGGAGGCTGGAGTGGATGGGGAATCATCATAGTGGAG 251
QY 181 GGCACCAACTACACCGCTCCCTCAAGAGTCGAGTGCAGTATTCATTCACAAGACAGCTCAA 240
Db 252 ---CACCAACTACACCGCTCCCTCAAGAGTCGAGTGCAGTATTCATTCACAAGACAGCTCAA 308
QY 241 GAACCAAGTTCCTCCCTGAACCTGAACTCTGTGACCGCCGCGACACGCGCGTATTACTG 300
Db 309 GAAGCAGCTCTCCCTGAAGTTGAGCTCTGTGACCGCCGCGGACCGCTGTGTATTACTG 369
QY 301 TGCCAG 306
Db 369 TGCAG 374
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RESULT 11

BI225611

LOCUS

DEFINITION

602948938F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:5093504 5',

mRNA sequence.

ACCESSION

BI225611

BI225611

602948938F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:5093504 5',

mRNA sequence.

ACCESSION

BI225611

VERSION B1225611.1 GI:14679055
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 365)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LICM1860 row: k column: 09
 High quality sequence stop: 365.
 Location/Qualifiers
 1..365
 /organism="Homo sapiens"
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 /db_xref="taxon:9606"
 /clone="IMAGE:5093504"
 /tissue_type="Burkitt lymphoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_8"
 /note="Organ: lymph; Vector: pOT87; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCAAGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."
 ORIGIN
 Query Match 55.2%; Score 207.6; DB 12; Length 365;
 Best Local Similarity 83.9%; Pred. No. 1.6e-43;
 Matches 260; Conservative 0; Mismatches 44; Indels 6; Gaps 2;
 QY 1 GGTCCTGCCAGCTGCAGCTGCAGGAGTGGGCGCCAGGAGTGGTGAAGCTTCGGAGAC 60
 Db 55 GGTCCTGCCAGCTGCAGCTGCAGGAGTGGGCGCCAGGAGTGGTGAAGCTTCGGAGAC 114
 QY 61 CCTGTCCCTCAGCTGCAGCTGCAGGAGTGGGCGCCAGGAGTGGTGAAGCTTCGGAGAC 120
 Db 115 CCTGTCCCTCAGCTGCAGCTGCAGGAGTGGGCGCCAGGAGTGGTGAAGCTTCGGAGAC 171
 QY 121 GATCCGCGAGCCCGGAGGAGTGGGCGCCAGGAGTGGTGAAGCTTCGGAGAC 180
 Db 172 GATCCGCGAGCCCGGAGGAGTGGGCGCCAGGAGTGGTGAAGCTTCGGAGAC 231
 QY 181 GGCCACCAATACAAACCGCTCCCTCAAGAGTGCAGTGCATCATTTCAAGACACGTCMA 240
 Db 232 ---CAACCAATACAAACCGCTCCCTCAAGAGTGCAGTGCATCATTTCAAGACACGTCMA 288
 QY 241 GAACAGATTCTCCCTGAACCTGAACCTGTGACACGCGCGGACACGCGCGTGTATTACTG 300
 Db 289 GAACAGATTCTCCCTGAAGTTGAGCTCTGTGAACGCGCGGACACGCGCGTGTATTACTG 348
 QY 301 TGCCAGAGAT 310
 Db 349 TGCAGAGAT 358
 RESULT 12
 AW503526
 LOCUS
 DEFINITION UI-HP-BN0-aky-b-04-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone
 340 bp mRNA linear EST 01-MAR-2000
 AW503526
 LOCUS
 DEFINITION UI-HP-BN0-aky-b-04-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone

IMAGE:3078487 5', mRNA sequence.
 AW503526
 VERSION AW503526.1 GI:7140086
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 340)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Eco RI site shown at the beginning of the sequence.
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: M.B. Soares Lab
 cDNA Library Arrayed by: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: M13 Forward.
 Location/Qualifiers
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 /clone="IMAGE:3078487"
 /tissue_type="lymph"
 /cell_type="germinal center B cells"
 /cell_line="MGC85"
 /lab_host="DH10B (lrf)"
 /clone_lib="NIH_MGC_50"
 /note="Vector: pT73-Pac; Site 1: NotI; Site 2: Eco RI;
 Constructed from size fractionated cytoplasmic mRNA
 (3.5-4.4kb). Directionally cloned. Cells provided by
 Louis M. Staudt, Ph.D. Library preparation by Maria de
 Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
 ORIGIN
 Query Match 55.1%; Score 207.2; DB 10; Length 340;
 Best Local Similarity 84.1%; Pred. No. 2e-43;
 Matches 259; Conservative 0; Mismatches 43; Indels 6; Gaps 2;
 QY 1 GGTCTGTCCAGCTGCAGCTGCAGGAGTGGGCGCCAGGAGTGGTGAAGCTTCGGAGAC 60
 Db 32 GGTCTGTCCAGCTGCAGCTGCAGGAGTGGGCGCCAGGAGTGGTGAAGCTTCGGAGAC 91
 QY 61 CCTGTCCCTCAGCTGCAGCTGCAGGAGTGGGCGCCAGGAGTGGTGAAGCTTCGGAGAC 117
 Db 92 CCTGTCCCTCAGCTGCAGCTGCAGGAGTGGGCGCCAGGAGTGGTGAAGCTTCGGAGAC 151
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 Db 152 CTGGATCCGCGAGCCCGGAGGAGTGGGCGCCAGGAGTGGTGAAGCTTCGGAGAC 208
 QY 178 TGGGGCCACCAACTACAAACCGCTCCCTCAAGAGTGCAGTGCATCATTTCAAGACACGTC 237
 Db 209 TGGAGACCACTACTACACACCGCTCCCTCCAGAGTGCAGTGCATCATTTCAAGACACGTC 268
 QY 238 CAAGACCAAGTTCTCTCCCTGAACCTGAACCTGTGACACGCGCGGACACGCGCGTGTATT 297
 Db 269 CAAGACCAAGTTCTCTCCCTGGATCTGAGCTCAGTACCGCGCGGACACGCGCGCTTTATTA 328
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 Db 329 TTGTGGA 336
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 LOCUS
 DEFINITION BF767440 361 bp mRNA linear EST 12-JAN-2001

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DEFINITION CM1-CN0061-131200-642-c02 CN0061 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF767440
VERSION BF767440.1 GI:12115340
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 361)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.P.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Sucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,P., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=CM1st2-CN1-CN0061-
131200-642-c02&t3=2000-12-13&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 360.
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/dev_stage="Adult"
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/note="Organ: colon normal; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No.196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
ORIGIN
Query Match 55.1%; Score 207; DB 10; Length 361;
Best Local Similarity 86.6%; Pred. No. 2.3e-43;
Matches 252; Conservative 0; Mismatches 35; Indels 4; Gaps 2;
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QY 61 CTTGTCTCTACCTCGCTGTCTCTGTGTGGCTCTGTGTGAGCTAGTACTGTGTGACCTG 120
Db 134 CTTGTCTCTACCTCGCTGTCTCTGTGTGGCTCTGTGTGAGCTAGTACTGTGTGAGCTG 193
QY 121 GATCC-GCCAGCCCGCCAGGAGCTGCAGTGTGAGTGTGAGTGTATCTCTGTGTGTGTG 179
Db 194 GGTCTGTGCGCCCGCCAGGAGGCGCTGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 250
QY 180 GGGCCACCAACTACAAACCGCTCTCTCAAGAGTCGAGTGTATCATTTTCAAGACAGCTCCA 239
Db 251 GGAGCACCACACTTCAACCGCTCTCTCAAGAGTCGAGTGTGAGTGTGAGTGTGAGTGTG 310
QY 240 AGAACCACTTCTCCCTGAGCACTGAACTCTGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 290
Db 311 AGAACCACTTCTCCCTGAGCACTGAACTCTGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 361
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RESULT 14
LOCUS CD704336
DEFINITION EST20863 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION CD704336
VERSION CD704336.1 GI:32234966
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 347)
AUTHORS Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and
Zeng,Y.-X.
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: YiXin Zeng
Cancer Center
Sun Yat-sen University
651 DongPeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gzsums.edu.cn.
FEATURES
Location/Qualifiers
1..347
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA
library from southern Chinese"
ORIGIN
Query Match 54.9%; Score 206.6; DB 14; Length 347;
Best Local Similarity 86.6%; Pred. No. 2.9e-43;
Matches 240; Conservative 0; Mismatches 34; Indels 3; Gaps 1;
QY 1 GGTCTGTCTCCAGCTGCAGCTGCAGAGTCGGGCCAGGAGTCGTGTGAGCCCTTCGGAGAC 60
Db 74 GGTCTGTCTCAGTGCAGCTGCAGAGTCGGGCCAGGAGTCGTGTGAGCCCTTCGGAGAC 133
QY 61 CTTGTCTCTACCTCGCTGTCTCTGTGTGGCTCTGTGTGAGCTAGTACTGTGTGAGCTG 120
Db 134 CTTGTCTCTACCTCGCTGTCTCTGTGTGGCTCTGTGTGAGCTAGTACTGTGTGAGCTG 193
QY 121 GATCCGCCAGCCCGCCAGGAGGAGTGTGAGTGTGAGTGTATCTCTGTGTGTGTG 180
Db 194 GGTCTGTGCGCCCGCCAGGAGGCGCTGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 250
QY 181 GGGCCACCAACTACAAACCGCTCTCTCAAGAGTCGAGTGTATCATTTTCAAGACAGCTCCA 240
Db 251 GAGCACCACACTACAAACCGCTCTCTCAAGAGTCGAGTGTATCATTTTCAAGACAGCTCCA 310
QY 241 GAACCACTTCTCCCTGAGCACTGAACTCTGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 277
Db 311 GAACCACTTCTCCCTGAGCACTGAACTCTGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 347
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DEFINITION bb20805 Y1 NIH MGC 8 Homo sapiens cDNA clone IMAGE:2963456 5',
similar to gb:M54911_rnal IG HEAVY CHAIN PRECURSOR V-II REGION
(HUMAN);, mRNA sequence.
ACCESSION AW733058
VERSION AW733058.1 GI:7633401
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Search completed: June 19, 2004, 07:31:24
Job time : 1737 secs

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2004, 04:01:44 ; Search time 1844 Seconds
(without alignments)
7545.073 Million cell updates/sec

Title: US-09-019-441A-5_COPY_67_387
Perfect score: 321
Sequence: 1 gacatccagatgaccagtc.....ggaccaagg-ggaaatcaaa 321

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 2865150

Minimum DB seq length: 0
Maximum DB seq length: 321

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

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- 2: gb htg.*
- 3: gb in.*
- 4: gb om.*
- 5: gb ov.*
- 6: gb pat.*
- 7: gb ph.*
- 8: gb pl.*
- 9: gb pr.*
- 10: gb ro.*
- 11: gb sts.*
- 12: gb sy.*
- 13: gb un.*
- 14: gb vi.*
- 15: em ba.*
- 16: em fun.*
- 17: em hum.*
- 18: em in.*
- 19: em mu.*
- 20: em om.*
- 21: em or.*
- 22: em ov.*
- 23: em pat.*
- 24: em ph.*
- 25: em pl.*
- 26: em ro.*
- 27: em sts.*
- 28: em un.*
- 29: em vi.*
- 30: em htg hum.*
- 31: em htg inv.*
- 32: em htg other.*
- 33: em htg mus.*
- 34: em htg pin.*
- 35: em htg rod.*
- 36: em htg mam.*
- 37: em htg vrt.*
- 38: em sv.*
- 39: em htgo hum.*
- 40: em htgo mus.*
- 41: em htgo other.*

Pred. No. is the number of results predicted by chance to have a

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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2	279.4	87.0	321	9	AY240164	AY240164 Homo sapi
3	273.2	85.1	311	9	HSA243111	AJ243111 Homo sapi
4	271.4	84.5	321	9	AF329459	AF329459 Homo sapi
5	271	84.4	320	9	HSA0408420	AJ408420 Homo sapi
6	270.4	84.2	313	9	AY062340	AY062340 Homo sapi
7	270	84.1	318	9	AF103418	AF103418 Homo sapi
8	269.8	84.0	321	9	AF090357	AF090357 Homo sapi
9	269.8	84.0	321	9	AF090357	L26035 Homo sapien
10	269.6	84.0	318	12	AF044451	AF044451 Synthetic
11	269.6	84.0	321	6	AR160973	AR160973 Sequence
12	269.6	84.0	321	6	AR161046	AR161046 Sequence
13	269.6	84.0	321	6	AR161049	AR161050 Sequence
14	269.6	84.0	321	6	AR161050	AJ408417 Homo sapi
15	269.4	83.9	320	9	HSA0408417	AY240163 Homo sapi
16	268.2	83.6	321	9	AY240163	AF044454 Synthetic
17	268	83.5	318	12	AF044454	AR160976 Sequence
18	268	83.5	321	6	AR160976	AR160976 Homo sapi
19	266.8	83.1	319	9	AF103383	AF103383 Sequence 47
20	266.6	83.1	315	6	A68531	A68531 Sequence 47
21	266.6	83.1	315	9	HSLD217VL	Y08249 H. sapiens m
22	266.6	83.1	321	6	AX354835	AX354835 Sequence
23	266.6	83.1	321	9	AF442762	AF442762 Homo sapi
24	266.6	83.1	321	9	HSSIA15VL	Z46311 H. sapiens i
25	266.4	83.0	318	12	AF044456	AF044456 Synthetic
26	266.4	83.0	321	6	AR160978	AR160978 Sequence
27	266.4	83.0	321	6	AR161044	AR161044 Sequence
28	265	82.6	314	9	AY062338	AY062338 Homo sapi
29	265	82.6	321	9	AY240165	AY240165 Homo sapi
30	264.8	82.5	318	12	AF044447	AF044447 Synthetic
31	264.8	82.5	318	12	AF044453	AF044453 Synthetic
32	264.8	82.5	321	6	AR160969	AR160969 Sequence
33	264.8	82.5	321	6	AR160975	AR160975 Sequence
34	264.8	82.5	321	6	AR161035	X98988 H. sapiens r
35	264.2	82.3	311	9	HSX98988	AY062339 Homo sapi
36	264	82.2	313	9	AY082339	AY315905 Synthetic
37	264	82.2	321	12	AY315905	E12913 Human cDNA
38	263.4	82.1	321	6	E12913	AX522255 Sequence
39	263.4	82.1	321	6	AX522255	AF306388 Homo sapi
40	262.8	81.9	318	9	AF306388	A68499 Sequence 15
41	261.8	81.6	315	6	A68499	Y08196 H. sapiens m
42	261.8	81.6	315	9	HSLD110VL	X29589 H. sapiens c
43	261.8	81.6	321	6	A29589	BD097618 Antibody
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ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION HSA0408402 320 bp DNA linear PRI 01-AUG-2001
Homo sapiens partial IGKV gene for immunoglobulin kappa chain
variable region, clone 7.
ACCESSION AJ408402
VERSION AJ408402.1 GI:12655491
KEYWORDS IGKV gene; immunoglobulin kappa chain; immunoglobulin light chain;
variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 320)
AUTHORS Harfst,E., Cooper,S., Neubauer,S., Distel,L. and Grawunder,U.

TITLE Normal V(D)J recombination in cells from patients with Nijmegen
breakage syndrome
JOURNAL Mol. Immunol. 37 (15), 915-929 (2000)
MEDLINE 21179652
PUBMED 11282395
REFERENCE 2 (bases 1 to 320)
AUTHORS Harfst, E.
TITLE Direct Submission
JOURNAL Submitted (04-JAN-2001) Harfst E., Immunologie,
Universitätsklinikum Ulm, Albert-Einstein-Allee 115 D-89081 Ulm,
GERMANY

FEATURES

Location/Qualifiers

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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="7"
/cell_type="B cell"
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/rearranged
/note="Nijmegen breakage syndrome (NBS) patient"

gene

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/gene="IGKV"

CDS

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/codon_start=2
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/db_xref="EMBL:CAC27598"
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/product="immunoglobulin kappa chain variable region"

ORIGIN

Query Match 87.4%; Score 280.6; DB 9; Length 320;
Best Local Similarity 92.5%; Pred. No. 6.2e-79;
Matches 295; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
QY 3 CATCAGATGACCCAGTCTCCATCTTCCTGTCATCTGTAGGGACAGATCAACAT 62
DB 1 CATCAGATGACCCAGTCTCCATCTTCCTGTCATCTGTAGGACAGATCAACAT 60
QY 63 CACTTGCAGGGCAGTCAGGACATAGGTATTTAAATTTGTATCAGCAGAACCCAGG 122
DB 61 CACTTGCAGGGCAGTCAGGACATAGAAATGATTTAGGCTGGTATCAGCAGAACCCAGG 120
QY 123 ABAAGCTCTAGCTTCCTGATCTATGTTGCATCCAGTTTGCAGTGGGTCCTCATCAAG 182
DB 121 GAAAGCCCTTAAGCCCTGATCTATGCTGCATCCAGTTTGCAGTGGGTCCTCATCAAG 180
QY 183 GTTCAGCGCAGTGGATCTGGGACAGAGTTCACTCTCCAGTCAGCAGCCTGCAGCCTGA 242
DB 181 GTTCAGCGCAGTGGATCTGGGACAGAGTTCACTCTCAACATCAGCAGCCTGCAGCCTGA 240
QY 243 AGATTTGGCACTTATTAATCTGTACAGGTTTATAGTACCCCTGGAGGTTGGGCCAAGG 302
DB 241 AGATTTGGCACTTATTAATCTGTACAGGTTTATAGTACCCCTGGAGGTTGGGCCAAGG 300
QY 303 GACCAAGGTGGAATCAAA 321
DB 301 GACCAAGGTGGAATCAAA 319

RESULT 2

AY240164
LOCUS
DEFINITION Homo sapiens clone HA6 anti-HAV capsid immunoglobulin G light chain
variable region mRNA, partial cds.
ACCESSION AY240164

VERSION AY240164.1 GI:29650334

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 321)

AUTHORS

Kim, S.J., Jang, M.H., Stapleton, J.T., Yoon, S.O., Jeon, E.-S. and
Hong, H.J.

TITLE

Neutralizing Human Monoclonal Antibodies to Hepatitis A Virus
Recovered by Phage Display

JOURNAL

Unpublished

REFERENCE

2 (bases 1 to 321)

AUTHORS

Kim, S.J., Jang, M.H., Stapleton, J.T., Yoon, S.O., Jeon, E.-S. and
Hong, H.J.

TITLE

Direct Submission

JOURNAL

Submitted (20-FEB-2003) Antibody Engineering RU, Korea Research
Institute of Bioscience and Biotechnology, Yuseong, Daejeon 305-333,
Korea

FEATURES

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variable region"
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KVEIK"

CDS

Query Match 87.0%; Score 279.4; DB 9; Length 321;
Best Local Similarity 91.9%; Pred. No. 1.5e-78;
Matches 295; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
QY 1 GACATCCAGATGACCCAGTCTCCATCTTCCTGTCATCTGTAGGGACAGATCAAC 60
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DB 61 ATCACTTGCAGGGCAGTCAGGACATAGGATTTAAATTTGTATCAGCAGAACCA 120
QY 121 GGAAGCTCTTAAGCTTCCTGATCTATGTTGCATCCAGTTTGCAGTGGGTCCTCATCA 180
DB 121 GGAAGCTCTTAAGCTTCCTGATCTATGTTGCATCCAGTTTGCAGTGGGTCCTCATCA 180
QY 181 AGGTTTCAGCGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTGCAGCCT 240
DB 181 AGGTTTCAGTGGCAGTGGATCTGGGACAGAGTTTCACTCTCACCATCAGCAGCTTGCACCT 240
QY 241 GAAAGTTTTCGAGCTTATTACTGTCTACAGGTTTATAGTACCCCTCGAGGTTTCGGCCAA 300
DB 241 GAAAGTTTTCGAGCTTATTACTGTCTACAGGTTTATAGTACCCCTCGAGGTTTCGGCCAA 300
QY 301 GGGACCAAGGTGGAATCAAA 321
DB 301 GGGACCAAGGTGGAATCAAA 321

ORIGIN

Query Match 87.0%; Score 279.4; DB 9; Length 321;
Best Local Similarity 91.9%; Pred. No. 1.5e-78;
Matches 295; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
QY 1 GACATCCAGATGACCCAGTCTCCATCTTCCTGTCATCTGTAGGGACAGATCAAC 60
DB 1 GACATCCAGATGACCCAGTCTCCATCTTCCTGTCATCTGTAGGACAGATCAAC 60
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DB 61 ATCACTTGCAGGGCAGTCAGGACATAGGATTTAAATTTGTATCAGCAGAACCA 120
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DB 121 GGAAGCTCTTAAGCTTCCTGATCTATGTTGCATCCAGTTTGCAGTGGGTCCTCATCA 180
QY 181 AGGTTTCAGCGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTGCAGCCT 240
DB 181 AGGTTTCAGTGGCAGTGGATCTGGGACAGAGTTTCACTCTCACCATCAGCAGCTTGCACCT 240
QY 241 GAAAGTTTTCGAGCTTATTACTGTCTACAGGTTTATAGTACCCCTCGAGGTTTCGGCCAA 300
DB 241 GAAAGTTTTCGAGCTTATTACTGTCTACAGGTTTATAGTACCCCTCGAGGTTTCGGCCAA 300
QY 301 GGGACCAAGGTGGAATCAAA 321
DB 301 GGGACCAAGGTGGAATCAAA 321

RESULT 3

HSA243111
LOCUS
DEFINITION Homo sapiens partial mRNA for immunoglobulin light chain variable
region (a30 gene).
ACCESSION AJ243111
VERSION AJ243111.1 GI:5102680
KEYWORDS a30 gene; immunoglobulin light chain; variable region.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Elagib, K.E., Tengner, P., Levi, M., Jonsson, R., Thompson, K.M.,
Natvig, J.B. and Watren-Herlenius, M.
TITLE Immunoglobulin variable genes and epitope recognition of human
monoclonal anti-Ro 52-kd in primary Sjogren's syndrome
JOURNAL Arthritis Rheum. 42 (11), 2471-2481 (1999)
MEDLINE 20021514
PUBMED 10555043
REFERENCE 2 (bases 1 to 311)
AUTHORS Elagib, K.E.
TITLE Direct Submission
JOURNAL Submitted (14-JUN-1999) Elagib K.E., Laboratory for Rheumatology
Research, Institute of Immunology, Fr. Qvamsgate 1, N-172 Oslo,
NORWAY
FEATURES
source Location/Qualifiers
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1..311
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Query Match 85.1%; Score 273.2; DB 9; Length 311;
Best Local Similarity 92.6%; Pred. No. 1.5e-76;
Matches 287; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
QY 1 GACATCCAGATGACCCAGTCCCATCTCCCTGTCATCTGTAGGGGACAGATCAACC 60
DB 1 GACATCCAGATGACCCAGTCCCATCTCCCTGTCATCTGTAGGGGACAGATCAACC 60
QY 61 ATCACTTGCAGGGCAAGTCAGGCAATAGAAATGATTAGCTGTATCAGAGAAACCA 120
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QY 121 GGAAGAGCTCTAAGCTCCTGATCTGATCTGATCCAGTTTGCAGAGTGGGTCCCATCA 180
DB 121 GGAAGAGCTCTAAGCTCCTGATCTGATCTGATCCAGTTTGCAGAGTGGGTCCCATCA 180
QY 181 AGGTTTCAGGGCAGTGGATCTGGGACAGAGTTCACTCTCAGCGTCAGACGCTGCAGCCT 240
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QY 241 GAAATTTGGGACTTATTACTGTCACAGGTTTATAGTACCCCTCGGAGTTGGGCCAA 300
DB 241 GAAGATTTGCACTTATTACTGTCACAGGTTTATAGTACCCCTCGGAGTTGGGCCAA 300
QY 301 GGGACCAAGG 310
DB 301 GGGACCAAGG 310

LOCUS AF329459 321 bp mRNA linear PRI 19-MAY-2003
DEFINITION Homo sapiens clone SK-18 recombinant antibody light chain VL domain
mRNA, partial cds.
ACCESSION AF329459
VERSION AF329459.1 GI:12957385
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 321)
AUTHORS Paul, S., Karle, S., Luo, J., Gololobov, G., Nishiyama, Y., Planque, S.,
Burt, G., Thiagarajan, P., Tramontano, A. and Hanson, C.
TITLE Characterization of Lupus Antibodies to a Conserved Epitope of HIV
gp120
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 321)
AUTHORS Paul, S., Karle, S., Luo, J., Gololobov, G., Nishiyama, Y., Planque, S.,
Burt, G., Thiagarajan, P., Tramontano, A. and Hanson, C.
TITLE Direct Submission
JOURNAL Submitted (18-DEC-2000) Pathology and Laboratory Medicine,
University of Texas-Houston Medical School, 6431 Fannin, Houston,
TX 77030, USA
FEATURES
source Location/Qualifiers
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/mol_type="mRNA"
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/clone="SK-18"
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diester) and gp120"
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KVEIK"

Query Match 84.5%; Score 271.4; DB 9; Length 321;
Best Local Similarity 90.3%; Pred. No. 5.7e-76;
Matches 290; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
QY 1 GACATCCAGATGACCCAGTCCCATCTCCCTGTCATCTGTAGGGGACAGATCAACC 60
DB 1 GACATCCAGATGACCCAGTCCCATCTCCCTGTCATCTGTAGGGGACAGATCAACC 60
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QY 241 GAAATTTGGGACTTATTACTGTCACAGGTTTATAGTACCCCTCGGAGTTGGGCCAA 300
DB 241 GAAGATTTGCACTTATTACTGTCACAGGTTTATAGTACCCCTCGGAGTTGGGCCAA 300
QY 301 GGGACCAAGG 321
DB 301 GGGACCAAGG 321

RESULT 5
HSA408420 320 bp DNA linear PRI 01-AUG-2001
LOCUS Homo sapiens partial IGKV gene for immunoglobulin kappa chain
DEFINITION variable region, clone 25.
ACCESSION AJ408420
VERSION IGKV gene; immunoglobulin kappa chain; immunoglobulin light chain;
KEYWORDS variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 320)
AUTHORS Harfst, E., Cooper, S., Neubauer, S., Distel, L. and Grawunder, U.
TITLE Normal V(D)J recombination in cells from patients with Nijmegen
breakage syndrome
JOURNAL Mol. Immunol. 37 (15), 915-929 (2000)
MEDLINE 21179652
PUBMED 11282395
REFERENCE 2 (bases 1 to 320)
AUTHORS Harfst, E.
TITLE Direct Submission
JOURNAL Submitted (04-JAN-2001) Harfst E., Immunologie,
Universitaetsklinikum Ulm, Albert-Einstein-Allee 115 D-89081 Ulm,
GERMANY
FEATURES
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Best Local Similarity 90.6%; Pred. No. 7.7e-76;
Matches 289; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 3 CATCCAGATGACCCAGTCTCCATCTTCCCTGCTGCACTGTAGGGGACAGAGTCACCAT 62
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QY 63 CACTTCAGGCGCAGTGTCTGGACAGAGTTCACTCTACCCGTCAGACGACGCTGCA 122
DB 61 CACTTCGCGGCGCAGTGTCTGGACAGAGTTCACTCTACCCGTCAGACGACGCTGCA 120
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DB 121 GAAAGCCCTAAGCTCTGATCTATGTTGATCCAGTTTGCAAGTGGGGTCCCATCAAG 180
QY 183 GTTCAGGCGCAGTGTCTGGACAGAGTTCACTCTACCCGTCAGACGACGCTGCA 242
DB 181 GTTCAGGCGCAGTGTCTGGACAGAGTTCACTCTACCCGTCAGACGACGCTGCA 240

QY 243 AGATTTTGGAGTCTATTACTGTCTACAGTTTATAGTACCCCTCGAGCTTCGGCAAG 302
DB 241 AGATTTTGGAGTCTATTACTGTCTACAGTTTATAGTACCCCTCGAGCTTCGGCAAG 300
QY 303 GACCAAGGTGGAAATCAAA 321
DB 301 GACCAAGGTGGAAATCAAA 319
RESULT 6
AY062340 313 bp mRNA linear PRI 23-JAN-2002
LOCUS Homo sapiens clone 59/707 immunoglobulin light chain kappa variable
DEFINITION region mRNA, partial cds.
ACCESSION AY062340
VERSION AY062340.1 GI:18307283
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 313)
AUTHORS Vaisbourd, M., Ignatovich, O., Dremcheva, A., Karpas, A. and Winter, G.
TITLE Molecular characterization of human monoclonal antibodies derived
from fusions of tonsil lymphocytes with a human myeloma cell line
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 313)
AUTHORS Vaisbourd, M., Ignatovich, O., Dremcheva, A., Karpas, A. and Winter, G.
TITLE Direct Submission
JOURNAL Submitted (14-NOV-2001) MRC Laboratory of Molecular Biology, Hills
Road, Cambridge CB2 2QH, UK
FEATURES
source Location/Qualifiers
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IK"
ORIGIN
Query Match 84.2%; Score 270.4; DB 9; Length 313;
Best Local Similarity 91.7%; Pred. No. 1.2e-75;
Matches 286; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 10 ATGACCCAGTCTCCATCTTCCCTGCTGCACTGTAGGGGACAGAGTCACCATCTTGC 69
DB 1 ATGACCCAGTCTCCATCTTCCCTGCTGCACTGTAGGGGACAGAGTCACCATCTTGC 60
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QY 130 CCTAAGTCTCTGATCTATGTTGATCCAGTTTGCAAGTGGGGTCCCATCAAGTTTCA 189
DB 121 CCTAAGTCTCTGATCTATGTTGATCCAGTTTGCAAGTGGGGTCCCATCAAGTTTCA 180
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DB 181 GGCAGTGTCTGGACAGAGTTCACTCTCAGCTGACGAGCTTGAAGATTTT 240
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DB 241 GCAACTTACTGTCTACAGGTTTATAGTACCCCTCGAGCTTCGGCCCAAGGACCAAG 300

Db 181 CAGTGGATCTGGCACAGATTTCCTCCTCACCATCAGCAGCCTGACGCTGAAGATTTC 240

Qy 252 GACTTATTACTGTCTACAGGTTTANAGTACCCCTCGACGTTGCGCCAGGACCAAGGT 311

Db 241 AACTTATTACTGTCTACAGGTTTANAGTACCCCTCGACGTTGCGCCAGGACCAAGGT 300

Qy 312 GGAATCAAA 321

Db 301 GGAATCAAA 310

RESULT 8

AF090357 321 bp mRNA linear PRI 24-SEP-1998

LOCUS Homo sapiens clone G8 anti-mucini light chain variable region mRNA,

DEFINITION partial cds.

ACCESSION AF090357

VERSION AF090357.1 GI:3644021

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 321)

AUTHORS Andersson, E., Henderikx, P., Krambovitis, E., Hoogenboom, H.R. and Borrebaeck, C.A.K.

TITLE A tandem repeat of MUC1 core protein induces a weak in vitro immune response in human B cells

JOURNAL Unpublished

MEDLINE 2 (bases 1 to 321)

AUTHORS Andersson, E., Henderikx, P., Krambovitis, E., Hoogenboom, H.R. and Borrebaeck, C.A.K.

TITLE Direct Submission

JOURNAL Submitted (04-SEP-1998) Immunotechnology, Lund University, P.O. Box 7031, Lund 220 07, Sweden

FEATURES

source Location/Qualifiers

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/organism="Homo sapiens"

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KLLYASTLQSGVPSRFSGSGTDTLTITSLQPEDFATYVQQLNSPRTFGQGT

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V_region

ORIGIN

Query Match 84.0%; Score 269.8; DB 9; Length 321;

Best Local Similarity 90.0%; Pred. No. 1.9e-75;

Matches 289; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy 1 GACATCCAGATGACCCAGTCTCCATCTTCCTGTCTGTCATCTAGGGGACAGATCACC 60

Db 1 GACATCCAGATGACCCAGTCTCCATCTTCCTGTCTGTCATCTAGGGGACAGATCACC 60

Qy 61 ATCATTCCAGGGGAGTCAGACATTAGGTATTATTTAAATTTGGTATCAGCAGAAACCA 120

Db 61 ATCATTCCAGGGGAGTCAGACATTAGGTATTATTTAAATTTGGTATCAGCAGAAACCA 120

Qy 121 GGAATCAAA 321

Db 121 GGAATCAAA 310

Qy 181 AGTTTCAGGGGAGTCAGACATTAGGTATTATTTAAATTTGGTATCAGCAGAAACCA 180

Db 181 AGTTTCAGGGGAGTCAGACATTAGGTATTATTTAAATTTGGTATCAGCAGAAACCA 180

Qy 181 AGTTTCAGGGGAGTCAGACATTAGGTATTATTTAAATTTGGTATCAGCAGAAACCA 180

Db 181 AGTTTCAGGGGAGTCAGACATTAGGTATTATTTAAATTTGGTATCAGCAGAAACCA 180

Qy 310 GTGGAATCAAA 321

Db 301 GTGGAATCAAA 312

RESULT 7

AF103418 318 bp mRNA linear PRI 03-MAR-1999

LOCUS Homo sapiens isolate donor D clone D79K immunoglobulin kappa light

DEFINITION chain variable region mRNA, partial cds.

ACCESSION AF103418

VERSION AF103418.1 GI:4323899

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 318)

AUTHORS de Wildt, R.M., Hoet, R.M., van Venrooij, W.J., Tomlinson, I.M. and Winter, G.

TITLE Analysis of heavy and light chain pairings indicates that receptor editing shapes the human antibody repertoire

JOURNAL J. Mol. Biol. 285 (3), 895-901 (1999)

MEDLINE 99141350

PUBMED 9887257

REFERENCE 2 (bases 1 to 318)

AUTHORS de Wildt, R.M.T., Hoet, R.M.A., van Venrooij, W.J., Tomlinson, I.M. and Winter, G.

TITLE Direct Submission

JOURNAL Submitted (29-OCT-1998) Centre for Protein Engineering, MRC, Hills Road, Cambridge CB2 2QH, UK

FEATURES

source Location/Qualifiers

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KRTG"

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V_region

ORIGIN

Query Match 84.1%; Score 270; DB 9; Length 318;

Best Local Similarity 91.9%; Pred. No. 1.6e-75;

Matches 285; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

Qy 12 GACCATCTCCATCTTCCTGTCTGTCATCTAGGGGACAGATCACCATCCTGTCAG 71

Db 1 GACCATCTCCATCTTCCTGTCTGTCATCTAGGGGACAGATCACCATCCTGTCAG 60

Qy 72 GGCAGTCCAGGACATTAGGTATTATTTAAATTTGGTATCAGCAGAAACCAAGCTCC 131

Db 61 GGCAGTCCAGGACATTAGGTATTATTTAAATTTGGTATCAGCAGAAACCAAGCTCC 120

Qy 132 TAAGTCTCTGATCTATGTCATCCAGTTTGCAAGTGGGTCCCATCAGGTTTCAGCG 191

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VERSION			
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REFERENCE			
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RESULT 14
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DEFINITION Sequence 222 from patent US 6255455.
ACCESSION AR161050
VERSION AR161050.1 GI:16226467
KEYWORDS
SOURCE
    Unknown.
ORGANISM
    Unknown.
REFERENCE
    1 (bases 1 to 321)
AUTHORS
    Siege.,D.L.
TITLE
    Rh(D)-binding proteins and magnetically activated cell sorting
    method for production thereof
JOURNAL
    Patent: US 6255455-A 222 03-JUL-2001;
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VERSION	AJ408417				
KEYWORDS	IGKV gene; immunoglobulin kappa chain; immunoglobulin light chain; variable region.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 320)				
TITLE	Harfst, E., Cooper, S., Neubauer, S., Distel, L. and Grauwunder, U.				
JOURNAL	Normal V(D)J recombination in cells from patients with Nijmegen breakage syndrome				
MEDLINE	Mol. Immunol. 37 (15), 915-929 (2000)				
PUBMED	21179652				
REFERENCE	1182395				
AUTHORS	2 (bases 1 to 320)				
TITLE	Harfst, E.				
JOURNAL	Direct Submission				
FEATURES	Submitted (04-JAN-2001) Harfst E., Immunologie, Universitaetsklinikum Ulm, Albert-Sztein-Allee 11\$ D-89081 Ulm, GERMANY				
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OM nucleic - nucleic search, using sw model

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Title: US-09-019-441a-5_COPY_67_387

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Total number of hits satisfying chosen parameters: 4121650

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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9: Geneseqn2003cs:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	269.6	84.0	321	5	AAH68720 Human ant
2	269.6	84.0	321	5	AAH68723 Human ant
3	269.6	84.0	321	5	AAH68647 Human ant
4	269.6	84.0	321	5	AAH68724 Human ant
5	269.6	84.0	321	8	ACD45311 Anti-Rh(D
6	269.6	84.0	321	8	ACD45384 Anti-Rh(D
7	269.6	84.0	321	8	ACD45388 Anti-Rh(D
8	269.6	84.0	321	8	ACD45387 Anti-Rh(D
9	268.2	83.6	321	7	ABZ24183 Anti-EGFR
10	268	83.5	321	5	AAH68650 Human ant
11	268	83.5	321	5	AAH68652 Human ant
12	266.6	83.1	315	2	AAV19759 Antibody
13	266.6	83.1	321	6	ABA06023 Human mon
14	266.4	83.0	321	5	AAH68718 Human ant
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16	266.4	83.0	321	8	ACD45382 Anti-Rh(D
17	266.4	83.0	321	8	ACD45316 Anti-Rh(D
18	264.8	82.5	321	5	AAH68649 Human ant
19	264.8	82.5	321	5	AAH68643 Human ant
20	264.8	82.5	321	5	AAH68709 Human ant
21	264.8	82.5	321	8	ACD45307 Anti-Rh(D
22	264.8	82.5	321	8	ACD45313 Anti-Rh(D
23	264.8	82.5	321	8	ACD45373 Anti-Rh(D

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27	261.8	81.6	321	4	AAH47731 Nucleotid
28	261.8	81.6	321	4	AAH47735 Nucleotid
29	261.6	81.5	321	5	AAH68717 Human ant
30	261.6	81.5	321	5	AAH68719 Human ant
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33	261.6	81.5	321	8	ACD45383 Anti-Rh(D
34	261.6	81.5	321	8	ACD45381 Anti-Rh(D
35	260.2	81.1	315	2	AAV19757 Antibody
36	260.2	81.1	315	2	AAV19761 Antibody
37	260.2	81.1	321	6	AAH45699 Human end
38	260.2	81.1	321	6	ABA94337 MAB 63 11
39	260	81.0	321	5	AAH68713 Human ant
40	258.4	80.5	318	2	AAV19745 Antibody
41	258.4	80.5	321	5	AAH68654 Human ant
42	258.4	80.5	321	5	AAH68701 Human ant
43	258.4	80.5	321	5	AAH68701 Human ant
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ALIGNMENTS

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AAH68720
ID AAH68720 standard; DNA; 321 BP.

AC AAH68720;

DT 14-SEP-2001 (first entry)

XX Human anti-Rh(D) antibody clone SH49 nucleotide sequence.

XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;

KW red blood cell; Rh phenotype; diagnosis; therapeutic; ds.

XX Homo sapiens.

XX US6255455-B1.

XX 03-JUL-2001.

XX 29-JAN-1999; 99US-00240274.

XX 11-OCT-1986; 96US-0028550P.

PR 27-JUN-1997; 97US-00894045.

PR 10-APR-1998; 98US-0081380P.

(UYPE-) UNIV PENNSYLVANIA.

Siegel DL;

DR WPI; 2001-388931/41.

DR P-PSDB; AAG93663.

XX New isolated protein, preferably a human anti-Rh(D) antibody for use in diagnostics requiring a human instead of an animal antibody and in therapeutic medicine.

XX Example 3; Col 79; 162pp; English.

XX The present invention describes an isolated Rh(D) binding protein, preferably a human antibody, (I) having an amino acid sequence comprising one of the sequences (S) given in AAG93558 to AAG93669. (I) has immunostimulant activity, and can be used as an immune system stimulant. (I) can be used in diagnostic and therapeutic medicine. The antibodies are used in diagnostics that require human antibodies instead of animal antibodies, such as determine the Rh phenotype of human red blood cells. AAH68615 to AAH68726 represent the nucleotide sequence which encode

DR P-PSDB; AAG93590.
 XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
 PT diagnostics requiring a human instead of an animal antibody and in
 PT therapeutic medicine.
 XX
 XX Siegel DL;
 XX
 XX WPI; 2001-388931/41.
 DR P-PSDB; AAG93667.
 XX
 XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
 PT diagnostics requiring a human instead of an animal antibody and in
 PT therapeutic medicine.
 XX
 XX Example 3; Col 80; 162pp; English.
 XX
 XX The present invention describes an isolated Rh(D) binding protein,
 CC preferably a human antibody, (I) having an amino acid sequence comprising
 CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
 CC immunostimulant activity, and can be used as an immune system stimulant.
 CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
 CC are used in diagnostics that require human antibodies instead of animal
 CC antibodies, such as determine the Rh phenotype of human red blood cells.
 CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
 CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
 CC chain CDR3 amino acid sequences which are given in the exemplification of
 CC the present invention
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 Best Local Similarity 90.8%; Pred. No. 1.1e-78;
 Matches 287; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
 QY 6 CCAGATGACCCAGTCTCCATCTCCCTGCTGTCATCTGTAGGGGACAGAGTCAACATCAC 65
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 XX 14-SEP-2001 (first entry)
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 XX Human anti-Rh(D) antibody clone SH54 nucleotide sequence.
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 XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
 KW red blood cell; Rh phenotype; diagnosis; therapeutic; ds.
 XX
 XX Homo sapiens.
 OS
 XX US6255455-B1.
 PN
 XX 03-JUL-2001.
 PD
 XX 29-JAN-1999; 99US-00240274.
 PF
 XX 11-OCT-1996; 96US-0028550P.
 PR

PR 27-JUN-1997; 97US-00884045.
 PR 10-APR-1998; 98US-0081380P.
 XX
 XX (UYPE-) UNIV PENNSYLVANIA.
 PA
 XX Siegel DL;
 PI
 XX WPI; 2001-388931/41.
 DR P-PSDB; AAG93667.
 XX
 XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
 PT diagnostics requiring a human instead of an animal antibody and in
 PT therapeutic medicine.
 XX
 XX Example 3; Col 80; 162pp; English.
 XX
 XX The present invention describes an isolated Rh(D) binding protein,
 CC preferably a human antibody, (I) having an amino acid sequence comprising
 CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
 CC immunostimulant activity, and can be used as an immune system stimulant.
 CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
 CC are used in diagnostics that require human antibodies instead of animal
 CC antibodies, such as determine the Rh phenotype of human red blood cells.
 CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
 CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
 CC chain CDR3 amino acid sequences which are given in the exemplification of
 CC the present invention
 XX
 XX Sequence 321 BP; 86 A; 86 C; 76 G; 73 T; 0 U; 0 Other;
 SQ
 Query Match 84.0%; Score 269.6; DB 5; Length 321;
 Best Local Similarity 90.8%; Pred. No. 1.1e-78;
 Matches 287; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
 QY 6 CCAGATGACCCAGTCTCCATCTCCCTGCTGTCATCTGTAGGGGACAGAGTCAACATCAC 65
 DB 3 CGAGCTCACCAGTCTCCATCTCCCTGCTGTCATCTGTAGGGGACAGAGTCAACATCAC 62
 QY 66 TTGCGGGCAAGTCAAGACATAGTATTAATTTAAATGCTATCAGCAGAAACCGAGGAA 125
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 DB 303 CAAGGTGGAATCAAA 318
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 AC ACD45311 standard; DNA; 321 BP.
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 XX ACD45311;
 AC
 XX 12-SEP-2003 (first entry)
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 XX Anti-Rh(D) chain I02 DNA.
 DE
 XX Human; ds; Gene; RH(D) binding protein; blood typing; blood product;
 KW magnetically activated cell sorting.
 XX
 XX Homo sapiens.
 OS

XX OS Homo sapiens.
 XX PN US2003040605-A1.
 XX PD 27-FEB-2003.
 XX PF 04-MAY-2001; 2001US-00848798.
 XX PR 11-OCT-1996; 96US-0028550P.
 XX PR 27-JUN-1997; 97US-00884045.
 XX PR 10-APR-1998; 98US-0081380P.
 XX PR 29-JAN-1999; 99US-00240274.
 XX PA (UTYPE-) UNIV PENNSYLVANIA.
 XX PI Siegel DL;
 XX DR WPI; 2003-512273/48.
 XX DR P-PSDB; ABO27470.
 XX PT New human Rh(D)-binding protein useful for various diagnostic and
 PT therapeutic applications, including typing of blood or blood products.
 XX PS Claim 12; Page 39; 187pp; English.
 XX CC The invention relates to an isolated Rh(D) binding protein. The protein
 CC can be used for magnetically activated cell sorting. The protein is
 CC useful in various diagnostic and therapeutic applications in humans,
 CC including typing of blood or blood products. The present sequence
 CC represents DNA encoding a human anti-Rh(D) chain
 XX SQ Sequence 321 BP; 86 A; 86 C; 76 G; 73 T; 0 U; 0 Other;
 Query Match 84.0%; Score 269.6; DB 8; Length 321;
 Best Local Similarity 90.8%; Pred. No. 1.1e-78;
 Matches 287; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
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 QY 306 CAAGTGGAAATCAAA 321
 Db 303 CAAGTGGAAATCAAA 318

RESULT 6
 ACD45384
 ID ACD45384 standard; DNA; 321 BP.
 XX AC ACD45384;
 XX AC ACD45384;
 XX DT 12-SEP-2003 (first entry)
 XX DE Anti-Rh(D) light chain SH49 DNA.
 XX KW Human; ds; gene; RH(D) binding protein; blood typing; blood product;
 XX magnetically activated cell sorting.

XX OS Homo sapiens.
 XX PN US2003040605-A1.
 XX PD 27-FEB-2003.
 XX PF 04-MAY-2001; 2001US-00848798.
 XX PR 11-OCT-1996; 96US-0028550P.
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 XX PR 10-APR-1998; 98US-0081380P.
 XX PR 29-JAN-1999; 99US-00240274.
 XX PA (UTYPE-) UNIV PENNSYLVANIA.
 XX PI Siegel DL;
 XX DR WPI; 2003-512273/48.
 XX DR P-PSDB; ABO27470.
 XX PT New human Rh(D)-binding protein useful for various diagnostic and
 PT therapeutic applications, including typing of blood or blood products.
 XX PS Claim 12; Page 61; 187pp; English.
 XX CC The invention relates to an isolated Rh(D) binding protein. The protein
 CC can be used for magnetically activated cell sorting. The protein is
 CC useful in various diagnostic and therapeutic applications in humans,
 CC including typing of blood or blood products. The present sequence
 CC represents DNA encoding a human anti-Rh(D) chain
 XX SQ Sequence 321 BP; 85 A; 87 C; 77 G; 72 T; 0 U; 0 Other;
 Query Match 84.0%; Score 269.6; DB 8; Length 321;
 Best Local Similarity 90.8%; Pred. No. 1.1e-78;
 Matches 287; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
 QY 6 CCAGATGACCCAGTCTCCATCTCCCTGTCGATCTCTAGGGGACAGAGTCACCATCAC 65
 Db 3 CGAGCTCACCCAGTCTCCATCTCCCTGTCGATCTCTAGGGGACAGAGTCACCATCAC 62
 QY 66 TTGCGGGCAGTCAGGACGATTTAGTATTATTTAAATTTGGTATCAGCAGAAACAGGAAA 125
 Db 63 TTGCGGGCAGTCAGGACGATTTAGTATTATTTAAATTTGGTATCAGCAGAAACAGGAAA 122
 QY 126 AGCTCTTAAGCTCTGATCTATGTTGCATCCAGTTTGCAAGTGGGTCCTCATCAAGGTT 185
 Db 123 AGCCCTTAAGCTCTGATCTATGTTGCATCCAGTTTGCAAGTGGGTCCTCATCAAGGTT 182
 QY 186 CAGCGGAGTGATCTGGGACAGAGTTCACTCTCAGCGTCAGCAGCCTGAGCTGAGA 245
 Db 183 CAGTGGCAGTGATCTGGGACAGAGTTCACTCTCAGCGTCAGCAGCCTGAGCTGAGA 242
 QY 246 TTTTGGCACTTATTACTGTCTACAGAGTTTATAGTACCCCTCGGAGCTTGGCCAGGGAC 305
 Db 243 TTTTGGCACTTATTACTGTCTACAGAGTTTATAGTACCCCTCGGAGCTTGGCCAGGGAC 302
 QY 306 CAAGTGGAAATCAAA 321
 Db 303 CAAGTGGAAATCAAA 318

RESULT 7
 ACD45388
 ID ACD45388 standard; DNA; 321 BP.
 XX AC ACD45388;
 XX AC ACD45388;
 XX DT 12-SEP-2003 (first entry)
 XX DE Anti-Rh(D) light chain SH54 DNA.
 XX KW

Search completed: June 19, 2004, 04:41:18
Job time : 277 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2004, 04:31:48 ; Search time 64 Seconds
(without alignments)
2783.426 Million cell updates/sec

Title: US-09-019-441A-5_COPY_67_387

Perfect score: 321
Sequence: 1 gacatccagatgacccagtc.....ggaccaaggtggaatacaaa 321

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 582709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 104408

Minimum DB seq length: 0
Maximum DB seq length: 321

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/prodata/2/ina/5A-COMB.seq: *
2: /cgn2_6/prodata/2/ina/5B-COMB.seq: *
3: /cgn2_6/prodata/2/ina/6A-COMB.seq: *
4: /cgn2_6/prodata/2/ina/6B-COMB.seq: *
5: /cgn2_6/prodata/2/ina/PCFUS-COMB.seq: *
6: /cgn2_6/prodata/2/ina/backfiles1.seq: *

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	269.6	84.0	321	3	US-09-240-274-102
2	269.6	84.0	321	3	US-09-240-274-216
3	269.6	84.0	321	3	US-09-240-274-221
4	269.6	84.0	321	3	US-09-240-274-222
5	268	83.5	321	3	US-09-240-274-105
6	266.4	83.0	321	3	US-09-240-274-107
7	266.4	83.0	321	3	US-09-240-274-216
8	264.8	82.5	321	3	US-09-240-274-98
9	264.8	82.5	321	3	US-09-240-274-104
10	264.8	82.5	321	3	US-09-240-274-207
11	261.8	81.6	321	2	US-08-378-939-13
12	261.6	81.5	321	3	US-09-240-274-201
13	261.6	81.5	321	3	US-09-240-274-215
14	261.6	81.5	321	3	US-09-240-274-217
15	260	81.0	321	3	US-09-240-274-211
16	258.4	80.5	321	3	US-09-240-274-109
17	258.4	80.5	321	3	US-09-240-274-199
18	257	80.1	321	1	US-08-488-376-12
19	257	80.1	321	2	US-08-634-223-12
20	257	80.1	321	2	US-08-634-224-12
21	257	80.1	321	2	US-08-634-400-12
22	257	80.1	321	2	US-08-635-878-12
23	257	80.1	321	2	US-08-770-057-12
24	257	80.1	321	3	US-09-335-697B-12
25	257	80.1	321	4	US-09-335-697B-12
26	257	80.1	321	4	US-09-740-002-12
27	256.8	80.0	321	3	US-09-240-274-113

28	256.8	80.0	321	3	US-09-240-274-102
29	253.6	79.0	321	3	US-09-240-274-205
30	253.6	79.0	321	3	US-09-240-274-106
31	253.6	79.0	321	3	US-09-240-274-200
32	252	78.5	321	3	US-09-240-274-213
33	250.6	78.1	321	3	US-08-599-226-36
34	250.6	78.1	321	3	US-09-125-098-36
35	250.6	78.1	321	3	US-09-540-018-36
36	250.4	78.0	321	3	US-09-240-274-114
37	240.8	75.0	318	3	US-09-240-274-208
38	236.2	73.6	321	4	US-09-560-198A-5
39	234.6	73.1	321	1	US-07-988-430-74
40	234.6	73.1	321	1	US-08-425-336-72
41	234.6	73.1	321	1	US-08-488-113B-72
42	234.6	73.1	321	1	US-08-477-484B-72
43	234.6	73.1	321	1	US-08-472-788A-76
44	234.6	73.1	321	2	US-08-646-360-72
45	234.6	73.1	321	2	US-08-082-842A-76

ALIGNMENTS

RESULT 1
US-09-240-274-102
; Sequence 102, Application US/09240274
; Patent No. 6253455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 102
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 102
US-09-240-274-102

Query Match Similarity 84.0%; Score 269.6; DB 3; Length 321;
Best Local Similarity 90.8%; Pred. No. 4.98-81;
Matches 287; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY	6	CCAGATGACCCAGTCTCCATCTTCCCTGCTCTGCACTCTGTAGGGACAGAGTCACCATCAC	65
Db	3	CGAGCTACCCAGTCTCCATCTTCCCTGCTCTGCACTCTGTAGGGACAGAGTCACCATCAC	62
QY	66	TTGAGGGCAAGTCAGGACATTAAGTATTTAAATTTGGTATCAGCGAAACCGAGAA	125
Db	63	TTGCGGGCAAGTCAGGACATTAAGTATTTAAATTTGGTATCAGCGAAACCGAGAA	122
QY	126	AGCTCTTAAGCTCTGATCTATGTTGCATCCAGTTTGCAGTTGGGGTCCCATCAAGTT	185
Db	123	AGCCCTTAAGCTCTGATCTATGTTGCATCCAGTTTGCAGTTGGGGTCCCATCAAGTT	182
QY	186	CAGCGGCAAGTGCATCTGGACAGAGTTCACTCTCACCGTCAGAGCCTGCAGCCTGAAGA	245
Db	183	CAGTGGCAGTGCATCTGGACAGAGTTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGA	242
QY	246	TTTTGGCACTTATTAAGTCTTACAGGTTTATAGTACCCCTGGAGCTTCGGCCAGGAC	305
Db	243	TTTTGCACTTATTAAGTCTTACAGGTTTATAGTACCCCTGGAGCTTCGGCCAGGAC	302
QY	306	CAAGGTGGAATCAAA	321

Db 63 TTCCGGGCAAGTCAGACATGGCACTTATTTAAATTTGGTATCAGCGAAACACGGGAA 122
Qy 126 AGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTCAAAAGTGGGTCCCATCAAGGTT 185
Db 123 AGCCCTAAGCTCCTGATCTATGTTGCATCCAGTTTCAAAAGTGGGTCCCATCAAGGTT 182
Qy 186 CAGCGGCAAGTGGGACAGAGGTTTCACTCTCAGCTCAGGAGCTTCCAGGCTGAAGA 245
Db 183 CAGTGGCAGTGGATCTGGGACAGATTTCACCTCACCATCAGCAGTCTGCACCTGAAGA 242
Qy 246 TTTTGGCAGTTTACTCTTACAGGTTTATAGTACCCCTCGGAGCTTGGCCCAAGGAC 305
Db 243 TTTTGGCACTTACTCTCAACAGAGTTTACAGTACCCCGTGGACGTTGGCCCAAGGAC 302
Qy 306 CAAGGTGGAATCAAA 321
Db 303 CAAGGTGGAATCAAA 318

RESULT 5
US-09-240-274-105
; Sequence 105, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald I.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 105
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I05
US-09-240-274-105

Query Match 83.5%; Score 268; DB 3; Length 321;
Best Local Similarity 90.5%; Pred. No. 1.7e-80;
Matches 286; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
Qy 6 CCAGATGACCCAGCTCCATCTTCCCTGCTGTCATCTGTAGGGGACAGAGTCACCATCAC 65
Db 3 CGAGCTCACCCAGTCTCCATCTCCCTGCTGTCATCTGTAGGAGACAGAGTCACCATCAC 62
Qy 66 TTGCGGGCAAGTCAGGACATTTAGGTATTTAAATTTGGTATCAGCGAAACACGGGAA 125
Db 63 TTGCGGGCAAGTCAGGACATTTAGGTATTTAAATTTGGTATCAGCGAAACACGGGAA 122
Qy 126 AGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTCAAAAGTGGGTCCCATCAAGGTT 185
Db 123 AGCCCTAAGCTCCTGATCTATGTTGCATCCAGTTTCAAAAGTGGGTCCCATCAAGGTT 182
Qy 186 CAGCGGCAAGTGGGACAGAGGTTTCACTCTCAGCTCAGGAGCTTCCAGGCTGAAGA 245
Db 183 CAGTGGCAGTGGATCTGGGACAGATTTCACCTCACCATCAGCAGTCTGCACCTGAAGA 242
Qy 246 TTTTGGCAGTTTACTCTTACAGGTTTATAGTACCCCTCGGAGCTTGGCCCAAGGAC 305
Db 243 TTTTGGCACTTACTCTCAACAGAGTTTACAGTACCCCGTGGACGTTGGCCCAAGGAC 302
Qy 306 CAAGGTGGAATCAAA 321
Db 303 CAAGGTGGAATCAAA 318

RESULT 6
US-09-240-274-107
; Sequence 107, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald I.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 107
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I07
US-09-240-274-107

Query Match 83.0%; Score 266.4; DB 3; Length 321;
Best Local Similarity 90.2%; Pred. No. 5.9e-80;
Matches 285; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
Qy 6 CCAGATGACCCAGCTCCATCTTCCCTGCTGTCATCTGTAGGGGACAGAGTCACCATCAC 65
Db 3 CGAGCTCACCCAGTCTCCATCTCCCTGCTGTCATCTGTAGGAGACAGAGTCACCATCAC 62
Qy 66 TTGCGGGCAAGTCAGGACATTTAGGTATTTAAATTTGGTATCAGCGAAACACGGGAA 125
Db 63 TTGCGGGCAAGTCAGGACATTTAGGTATTTAAATTTGGTATCAGCGAAACACGGGAA 122
Qy 126 AGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTCAAAAGTGGGTCCCATCAAGGTT 185
Db 123 AGCCCTAAGCTCCTGATCTATGTTGCATCCAGTTTCAAAAGTGGGTCCCATCAAGGTT 182
Qy 186 CAGCGGCAAGTGGGATCTGGGACAGATTTCACCTCACCATCAGCAGTCTGCACCTGAAGA 245
Db 183 CAGTGGCAGTGGATCTGGGACAGATTTCACCTCACCATCAGCAGTCTGCACCTGAAGA 242
Qy 246 TTTTGGCAGTTTACTCTTACAGGTTTATAGTACCCCTCGGAGCTTGGCCCAAGGAC 305
Db 243 TTTTGGCACTTACTCTCAACAGAGTTTACAGTACCCCGTGGACGTTGGCCCAAGGAC 302
Qy 306 CAAGGTGGAATCAAA 321
Db 303 CAAGGTGGAATCAAA 318

RESULT 7
US-09-240-274-216
; Sequence 216, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald I.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 216

LENGTH: 321
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH47
US-09-240-274-216

Query Match 83.0%; Score 266.4; DB 3; Length 321;
Best Local Similarity 90.2%; Pred. No. 5, 9e-80;
Matches 285; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 6 CCAGATGACCCAGTCTCCATCTCCCTGCTGTCATCTGTAGGGGACAGAGTCACCATCAC 65
DB 3 CGAGCTCACCCAGTCTCCATCTCCCTGCTGTCATCTGTAGGGGACAGAGTCACCATCAC 62
QY 66 TTGCGAGGCAAGTCAGGACATTAGGTATTATTAAATGGTATCAGCAGAAACAGGAAA 125
DB 63 TTGCGGGGCAAGTCAGGACATTAGGTATTATTAAATGGTATCAGCAGAAACAGGAAA 122
QY 126 AGCTCTAAGCTCTGATCTATGTCATCTTATAGTACCCCTCGGACGTTCCCATCAAGGTT 185
DB 123 AGCCCTAACTCTGATCTATGTCATCTTATAGTACCCCTCGGACGTTCCCATCAAGGTT 182
QY 186 CAGCGGCAAGTCAGGACAGGTTCACTCTCAGCGTCAGCAGCTGCGCAAGGGAC 245
DB 183 CAGTGGCAGTGGATCTGGGACAGATTCTCTCACCATCAGCATCTGCACTTGAAGA 242
QY 246 TTTTGGCACTTATTACTGTCACAGGTTTATAGTACCCCTCGGACGTTCCCATCAAGGTT 305
DB 243 TTTTGGCACTTATTACTGTCACAGGTTTATAGTACCCCTCGGACGTTCCCATCAAGGTT 302
QY 306 CAGGTGGAAATCAAA 321
DB 303 CAAGGTGGAGATCAGA 318

RESULT 8
US-09-240-274-98
Sequence 98, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-42U2
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 98
LENGTH: 321
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain F01
US-09-240-274-98

Query Match 82.5%; Score 264.8; DB 3; Length 321;
Best Local Similarity 89.9%; Pred. No. 2e-79;
Matches 284; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 6 CCAGATGACCCAGTCTCCATCTTCCCTGCTGTCATCTGTAGGGGACAGAGTCACCATCAC 65
DB 3 CGAGCTCACCCAGTCTCCATCTTCCCTGCTGTCATCTGTAGGGGACAGAGTCACCATCAC 62
QY 66 TTGCGAGGCAAGTCAGGACATTAGGTATTATTAAATGGTATCAGCAGAAACAGGAAA 125
DB 63 TTGCGGGGCAAGTCAGGACATTAGGTATTATTAAATGGTATCAGCAGAAACAGGAAA 122

QY 126 AGCTCTAAGCTCTGATCTATGTCATCTTATAGTACCCCTCGGACGTTCCCATCAAGGTT 185
DB 123 AGCCCTAACTCTGATCTATGTCATCTTATAGTACCCCTCGGACGTTCCCATCAAGGTT 182
QY 186 CAGCGGCAAGTCAGGACAGGTTCACTCTCAGCGTCAGCAGCTGCGCAAGGGAC 245
DB 183 CAGCGGCAAGTCAGGACAGGTTCACTCTCAGCGTCAGCAGCTGCGCAAGGGAC 242
QY 246 TTTTGGCACTTATTACTGTCACAGGTTTATAGTACCCCTCGGACGTTCCCATCAAGGTT 305
DB 243 TTTTGGCACTTATTACTGTCACAGGTTTATAGTACCCCTCGGACGTTCCCATCAAGGTT 302
QY 306 CAGGTGGAAATCAAA 321
DB 303 CAAGGTGGAGATCAGA 318

RESULT 9
US-09-240-274-104
Sequence 104, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-42U2
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 104
LENGTH: 321
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain I04
US-09-240-274-104

Query Match 82.5%; Score 264.8; DB 3; Length 321;
Best Local Similarity 89.9%; Pred. No. 2e-79;
Matches 284; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 6 CCAGATGACCCAGTCTCCATCTTCCCTGCTGTCATCTGTAGGGGACAGAGTCACCATCAC 65
DB 3 CGAGCTCACCCAGTCTCCATCTTCCCTGCTGTCATCTGTAGGGGACAGAGTCACCATCAC 62
QY 66 TTGCGAGGCAAGTCAGGACATTAGGTATTATTAAATGGTATCAGCAGAAACAGGAAA 125
DB 63 TTGCGGGGCAAGTCAGGACATTAGGTATTATTAAATGGTATCAGCAGAAACAGGAAA 122
QY 126 AGCTCTAAGCTCTGATCTATGTCATCTTATAGTACCCCTCGGACGTTCCCATCAAGGTT 185
DB 123 AGCCCTAACTCTGATCTATGTCATCTTATAGTACCCCTCGGACGTTCCCATCAAGGTT 182
QY 186 CAGCGGCAAGTCAGGACAGGTTCACTCTCAGCGTCAGCAGCTGCGCAAGGGAC 245
DB 183 CAGTGGCAGTGGATCTGGGACAGATTCTCTCACCATCAGCATCTGCACTTGAAGA 242
QY 246 TTTTGGCACTTATTACTGTCACAGGTTTATAGTACCCCTCGGACGTTCCCATCAAGGTT 305
DB 243 TTTTGGCACTTATTACTGTCACAGGTTTATAGTACCCCTCGGACGTTCCCATCAAGGTT 302
QY 306 CAGGTGGAAATCAAA 321
DB 303 CAAGGTGGAGATCAGA 318

RESULT 10
US-09-240-274-207

Sequence 207, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 207
LENGTH: 321
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH28
US-09-240-274-207

Query Match 82.5%; Score 264.8; DB 3; Length 321;
Best Local Similarity 89.9%; Pred. No. 2e-79;
Matches 284; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 6 CCAGATGACCCAGTCTGATCTCCCTGCTGATCTGAGGAGACAGAGTCAACATCAC 65
Db 3 CGAGCTCACCAGTCTCCATCTCCCTGCTGATCTGAGGAGACAGAGTCAACATCAC 62
QY 66 TTGCGGGCAGATCAGACAGATAGGATATTATTAATGATATCAGCAGAAACCCAGAAA 125
Db 63 TTGCGGGCAGATCAGACAGATAGGAGTCTTAAATGATATCAGCAGAAACCCAGAAA 122
QY 126 AGCTCTTAAGTCTGATCTATGTTGATCAGTTTGCAAGTGGGGTCCATCAAGTTT 185
Db 123 AGCCCTTAAGTCTGATCTATGTTGATCAGTTTGCAAGTGGGGTCCATCAAGTTT 182
QY 186 CAGCGGAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCTCGAGCTGAAGA 245
Db 183 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCACTGAAGA 242
QY 246 TTTTGGCACTTATCTGCTCAAGTTTATAGTACCCCTCGAGAGTTCGGCCCAAGGGAC 305
Db 243 TTTTGGCACTTATCTGCTCAAGTTTATAGTACCCCTCGAGAGTTCGGCCCAAGGGAC 302
QY 306 CAAGTGGAAATCAAA 321
Db 303 CAAGTGGAAATCAAA 318

RESULT 11
US-08-378-939-13
Sequence 13, Application US/08378939
Patent No. 5876361
GENERAL INFORMATION:
APPLICANT: CROME, JAMES SCOTT
APPLICANT: LEWIS, ALAN PETER
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
STREET: 555 THIRTEENTH ST. N.W.
CITY: WASHINGTON
STATE: D. C.
COUNTRY: U.S.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,939
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952640
FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, BARBARA G
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1808-118
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 783-6040
TELEFAX: (202) 783-6031
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 321 base pairs
TYPE: nucleic acid
STRANDEDNESS: Both
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..321
US-08-378-939-13

Query Match 81.6%; Score 261.8; DB 2; Length 321;
Best Local Similarity 88.5%; Pred. No. 2.1e-78;
Matches 284; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
QY 1 GACATCCAGATGACCCAGTCTCCATCTCCCTGCTGATCTGAGGAGACAGATCAC 60
Db 1 GACATCCAGATGACCCAGTCTCCATCTCCCTGCTGATCTGAGGAGACAGATCAC 60
QY 61 ATCACTTGGAGGGCAAGTCAGGACATTAGGATATTATTAATGATATCAGCAGAAACCA 120
Db 61 ATCACTTGGAGGGCAAGTCAGGACATTAGGATATTATTAATGATATCAGCAGAAACCA 120
QY 121 GAAAAAGCTCTAGCTCCTGATCTATGTTGATCCAGTTTGCAGAGTGGGGTCCCATCA 180
Db 121 GGGAAAGCTCTAGCTCCTGATCTATGTTGATCCAGTTTGCAGAGTGGGGTCCCATCA 180
QY 181 AGTTTCAGCGCAGTGGATCTGGGACAGAGTTCACCTCTCACCGTCAGCAGCTCGAGCCT 240
Db 181 AGTTTCAGCGCAGTGGATCTGGGACAGAGTTCACCTCTCACCGTCAGCAGCTCGAGCCT 240
QY 241 GAAGATTTGGGACTTATCTCTACAGTTTATAGTACCCCTCGAGCTTGGGCCAA 300
Db 241 GAAGATTTGGGACTTATCTCTACAGTTTATAGTACCCCTCGAGCTTGGGCCAA 300
QY 301 GGGACCAAGGTGGAAATCAAA 321
Db 301 GGGACCAAGGTGGAGATTAAA 321

RESULT 12
US-09-240-274-201
Sequence 201, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224

63	TTGCGGGCAAGTCAGTACATTAGCAGCTATTTTAAATTTGGTATCAGCAGAAACACGGGAA	122
Db		
126	AGCTCTTAAGCTCCTGATCTATGTGGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTT	185
Qy		
123	AGCCCTTAATCTCTCTGATCTATGCTGCATCCAGATTGCAAAAGTGGGGTCCCATCAAGGTT	182
Db		
186	CAGGGCAGTGGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTGCGACCTGAAGA	245
Qy		
183	CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCGAACCTGAAGA	242
Db		
246	TTTTGCGACTATTACTGTCTACAGGTTTATAGTACCCTCGGACGTTTCGGCCCAAGGAC	305
Qy		
243	TTTTGCAACTTACTACTGTCAACAGACTTACAGTTCCCTTAGCACTTTTCGGCCCTGGAC	302
Db		
306	CAAGGTGGAAATCAAA	321
Qy		
303	CAAAAGTGGATATCAAA	318
Db		

[illegible]

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RESULT 14
US-09-240-274-217
; Sequence 217, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 217
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH48
US-09-240-274-217

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; TYPE: DNA
; ORGANISM: Homo sapiens
;
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH48
US-09-240-274-217

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Query Match      81.5%;   Score 261.6;   DB 3;   Length 321;
Best Local Similarity 89.2%;   Pred. No. 2.4e-78;
Matches 282; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
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QY	6	CCAGATGACCCAGGCTCCATCTCTCCCTGTCTGGATCTGTAGGGGACAGAGTCCACCATCAC	65
DB	3	CGAGCTCACCAGGCTCCATCTCTCCCTGTCTGGATCTGTAGGAGACAGAGTCCACCATCAC	62
QY	66	TTGCAGGGCAAGTCAGGACATTAAGGTATTATTTTAAATTCGGTATCAGCAGAAACCAAGGAAA	125
DB	63	TTGCGGGCAAGTCAGGTACATTAGCAGCTATTTTAAATTCGGTATCAGCAGAAACCAAGGAAA	122
QY	126	AGCTCTTAAGCTCTCTGATCTATGTTGGATCCAGTTTGTGAAAGTGGGGTCCCATCAAGGTT	185
DB	123	AGCCCTTAATCTCTGTGATCTATGCTGGATCCAGTTTGTGAAAGTGGGGTCCCATCAAGGTT	182
QY	186	CAGCGGGCAGTGGATCTCGGACAGAGTTCACTCTCAACCGTCAGCAGCTCGAGCCTTGAAGA	245
DB	183	CAGTGGCAGTGGATCTCGGACAGATTCACTCTCAACCATCAGCAGTCTCTGCAACCTTGAAGA	242
QY	246	TTTTTGGACATTATTAATCTGTACAGGTTTATAGTACCCCTCGGACGTTTCGGCCCAAGGCAC	305
DB	243	TTTTTGCAACTTATCTATCTGTCAAAGACTTACAGTTCCCTTAGCACATTTTCGGCCCTGGAC	302
QY	306	CAAGGTGGAAATCAAA	321
DB	303	CAAAAGTGGATCAAA	318

245 TTTTGGCACTTTATFACGTCTACAGGTTTATAGTACCCCTCGACGTTTCGGCCACAGGAC 305
 QY
 246 TTTTGGCACTTTATFACGTCTACAGGTTTATAGTACCCCTCGACGTTTCGGCCACAGGAC 305
 QY
 243 TTTTGGCACTTTATFACGTCTACAGGTTTATAGTACCCCTCGACGTTTCGGCCACAGGAC 302
 Db
 306 CAAAGTGGAAATCAA 321
 QY
 303 CAAAGTGGATATCAA 318
 Db


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RESULT 15
US-09-240-274-211
; Sequence 211, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 211
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH36
US-09-240-274-211

Query Match      81.0%; Score 260; DB 3; Length 321;
Best Local Similarity 88.9%; Pred. No. 8.3e-78;
Matches 281; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 6 CCAGATGACCCAGTCTCCATCTTCCCTGCTGTCATCTGTAGGGGACAGAGTCACCATCAC 65
DB 3 CGAGCTCACTCAGTCTCCATCTCCCTGCTGTCATCTGTAGGAGACAGAGTCACCATCAC 62

QY 66 TTCACGGGCAAGTCAGACATTTAGGTATTTATTTATTTGTTATTCAGCAGAAACCCAGAAA 125
DB 63 TTCCCGGGCAAGTCAGACATTTAGGTATTTATTTATTTGTTATTCAGCAGAAACCCAGAAA 122

QY 126 AGCTCCTAAGCTCCTGATCTATCTGTCATCCAGTTTGCAAGTGGGGTCCCATCAAGGTT 185
DB 123 ATCCCTAAGCTCCTGATCTATCTGTCATCCAGTTTGCAAGTGGGGTCCCATCAAGGTT 182

QY 186 CAGCGGCAAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGGAGCTGCGGCTGAGAA 245
DB 183 CAGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAGTCTGCAACCTGAGAA 242

QY 246 TTTTGGGACTTATTACTGTCACAGTTTATAGTACCCCTCGGACGTTGCGGCAAGGGAC 305
DB 243 TTTTGGAACTTACTGTCACAGTTTATAGTACCCCTCGGACGTTTGGGCTTGGGCTGGGAC 302

QY 306 CAAGGTGGAAATCAAA 321
DB 303 CAAAGTGGATATCAAA 318

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Search completed: June 19, 2004, 05:42:26
Job time : 65 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2004, 05:12:14 ; Search time 284 Seconds
(Without alignments)
5177.921 Million cell updates/sec

Title: US-09-019-441a-5_COPY_67_387

Perfect score: 321
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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 2488216

Minimum DB seq length: 0
Maximum DB seq length: 321

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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- 3: /cgn2_6/prodata/2/pubpna/US06_NEW_PUB.seq:*
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- 10: /cgn2_6/prodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/prodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/prodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/prodata/2/pubpna/US09_NEW_PUB.seq:*
- 14: /cgn2_6/prodata/2/pubpna/US10A_PUBCOMB.seq:*
- 15: /cgn2_6/prodata/2/pubpna/US10B_PUBCOMB.seq:*
- 16: /cgn2_6/prodata/2/pubpna/US10C_PUBCOMB.seq:*
- 17: /cgn2_6/prodata/2/pubpna/US10_NEW_PUB.seq:*
- 18: /cgn2_6/prodata/2/pubpna/US60_NEW_PUB.seq:*
- 19: /cgn2_6/prodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	271.4	84.5	321	17	US-10-663-244-78
2	269.6	84.0	321	10	US-09-848-798-102
3	269.6	84.0	321	10	US-09-848-798-218
4	269.6	84.0	321	10	US-09-848-798-221
5	269.6	84.0	321	10	US-09-848-798-222
6	268.2	83.6	321	15	US-10-172-317-3
7	268.2	83.6	321	15	US-10-320-094-3
8	268	83.5	321	10	US-09-848-798-105
9	266.6	83.1	321	15	US-09-851-614-1
10	266.6	83.1	321	15	US-10-035-637-1
11	266.4	83.0	321	10	US-09-848-798-107
12	266.4	83.0	321	10	US-09-848-798-216
13	265	82.5	321	15	US-10-060-585-9
14	264.8	82.5	321	10	US-09-848-798-98

15	264.8	82.5	321	10	US-09-848-798-104
16	264.8	82.5	321	10	US-09-848-798-207
17	263.4	82.1	321	15	US-10-073-644C-3
18	261.6	81.5	321	10	US-09-848-798-201
19	261.6	81.5	321	10	US-09-848-798-215
20	261.6	81.5	321	10	US-09-848-798-217
21	260.2	81.1	321	13	US-10-363-349-9
22	260.2	81.1	321	15	US-10-324-493-21
23	260	81.0	321	10	US-09-848-798-211
24	258.4	80.5	321	10	US-09-848-798-109
25	258.4	80.5	321	10	US-09-848-798-199
26	257	80.1	321	9	US-09-740-002-12
27	257	80.1	321	16	US-10-173-551-28
28	257	80.1	321	16	US-10-384-356-12
29	257	80.1	321	17	US-10-325-698-12
30	256.8	80.0	321	10	US-09-848-798-113
31	256.8	80.0	321	10	US-09-848-798-205
32	255.4	79.6	321	13	US-10-221-529-3
33	255.4	79.6	321	15	US-10-091-300-32
34	253.8	79.1	318	8	US-08-844-215-20
35	253.8	79.1	321	15	US-10-091-300-36
36	253.8	79.1	321	17	US-10-663-244-82
37	253.6	79.0	321	10	US-09-848-798-106
38	253.6	79.0	321	10	US-09-848-798-200
39	253.6	79.0	321	10	US-09-848-798-213
40	252	78.5	321	10	US-09-848-798-103
41	250.6	78.1	302	17	US-10-038-591-9
42	250.6	78.1	321	10	US-09-801-185A-36
43	250.6	78.1	321	16	US-10-133-715-36
44	250.6	78.1	321	16	US-10-302-356A-36
45	250.6	78.1	321	16	US-10-163-657A-36

ALIGNMENTS

RESULT 1

US-10-663-244-78
; Sequence 78, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; PRIOR FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated oligonucleotide
US-10-663-244-78

QY	1	GACATCCAGATGACCCAGTCTCCATCTTCCTCGTCTGTCATCTGTAGGGACAGATCACC	60
DB	1	GACATCCAGATGACCCAGTCTCCATCTTCCTCGTCTGTCATCTGTAGGGACAGATCACC	60
QY	61	ATCATTCCAGGCGCAAGTCAGGATAGTATTATTTAAATTTGTTATCAGCAGAAACCA	120
DB	61	ATCATTCCAGGCGCAAGTCAGGATAGTATTATTTAAATTTGTTATCAGCAGAAACCA	120

QY 121 GGAAGAGCTCTAAGCTCTGATCTATGTTGATCCAGTTTGCAGAGTGGGGTCCCATCA 180
DB 121 GGAAGAGCTCTAAGCTCTGATCTATGTTGATCCAGTTTGCAGAGTGGGGTCCCATCA 180
QY 181 AGGTTTCAGCGGAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGAGCTGCAGCCT 240
DB 181 AGGTTTCAGCGGAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGAGCTGCAGCCT 240
QY 241 GAAGATTTCGCACTTATTACTGTCTACAGAGTTTATAGTACCCCTCGGAGCTTGGGCCAA 300
DB 241 GAAGATTTCGCACTTATTACTGTCTACAGAGTTTATAGTACCCCTCGGAGCTTGGGCCAA 300
QY 301 GGGACCAAGGTGGAATCAAA 321
DB 301 GGGACCAAGGTGGAATCAAA 321

RESULT 2

US-09-848-798-102
; Sequence 102, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 102
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 102
US-09-848-798-102

Query Match 84.0%; Score 269.6; DB 10; Length 321;
Best Local Similarity 90.8%; Pred. No. 5.1e-80;
Matches 287; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
QY 6 CCAGATGACCCAGTCTCCATCTCCCTCTGTCATCTGTAGGGGACAGAGTCACCATCAC 65
DB 3 CGAGCTCACCCAGTCTCCATCTCCCTCTGTCATCTGTAGGGGACAGAGTCACCATCAC 62
QY 66 TTGCGAGGCAAGTCAGGACATAGGTATTTAAATTTGGTATCAGCAGAACCGAGAA 125
DB 63 TTGCGGGCAAGTCAGGACATAGGTATTTAAATTTGGTATCAGCAGAACCGAGAA 122
QY 126 AGCTCTAAGCTCTGATCTATGTTGATCCAGTTTGCAGAGTGGGGTCCCATCAAGTT 185
DB 123 AGCCCTTAAGCTCTGATCTATGTTGATCCAGTTTGCAGAGTGGGGTCCCATCAAGTT 182
QY 186 CAGCGGAGTGGATCGGACAGAGTTCACTCTCACCGTCAGAGCTGCAGCTGAAGA 245
DB 183 CAGTGGCAGTGGATCGGACAGAGTTCACTCTCACCGTCAGAGCTGCAGCTGAAGA 242
QY 246 TTTTCGCACTTATTACTGTCTACAGAGTTTATAGTACCCCTCGGAGCTTGGGCCAAGGAC 305
DB 243 TTTTCGCACTTATTACTGTCTACAGAGTTTATAGTACCCCTCGGAGCTTGGGCCAAGGAC 302
QY 306 CAAGGTGGAATCAAA 321
DB 303 CAAGGTGGAATCAAA 318

RESULT 3

US-09-848-798-221
; Sequence 221, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 221
; LENGTH: 321
; TYPE: DNA

US-09-848-798-218
; Sequence 218, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 218
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-09-848-798-218

Query Match 84.0%; Score 269.6; DB 10; Length 321;
Best Local Similarity 90.8%; Pred. No. 5.1e-80;
Matches 287; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
QY 6 CCAGATGACCCAGTCTCCATCTCCCTCTGTCATCTGTAGGGGACAGAGTCACCATCAC 65
DB 3 CGAGCTCACCCAGTCTCCATCTCCCTCTGTCATCTGTAGGGGACAGAGTCACCATCAC 62
QY 66 TTGCGAGGCAAGTCAGGACATAGGTATTTAAATTTGGTATCAGCAGAACCGAGAA 125
DB 63 TTGCGGGCAAGTCAGGACATAGGTATTTAAATTTGGTATCAGCAGAACCGAGAA 122
QY 126 AGCTCTAAGCTCTGATCTATGTTGATCCAGTTTGCAGAGTGGGGTCCCATCAAGTT 185
DB 123 AGCCCTTAAGCTCTGATCTATGTTGATCCAGTTTGCAGAGTGGGGTCCCATCAAGTT 182
QY 186 CAGCGGAGTGGATCGGACAGAGTTCACTCTCACCGTCAGAGCTGCAGCTGAAGA 245
DB 183 CAGTGGCAGTGGATCGGACAGAGTTCACTCTCACCGTCAGAGCTGCAGCTGAAGA 242
QY 246 TTTTCGCACTTATTACTGTCTACAGAGTTTATAGTACCCCTCGGAGCTTGGGCCAAGGAC 305
DB 243 TTTTCGCACTTATTACTGTCTACAGAGTTTATAGTACCCCTCGGAGCTTGGGCCAAGGAC 302
QY 306 CAAGGTGGAATCAAA 321
DB 303 CAAGGTGGAATCAAA 318

RESULT 4
US-09-848-798-221
; Sequence 221, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 221
; LENGTH: 321
; TYPE: DNA

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; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH52
US-09-848-798-221

Query Match      84.0%; Score 269.6; DB 10; Length 321;
Best Local Similarity 90.8%; Pred. No. 5.1e-80;
Matches 287; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 6 CCAGATGACCCAGTCTCCATCTTCCTGTCGATCTGTAGGGACAGAGTCACCATCAC 65
DB 3 CGAGCTCACCCAGTCTCCATCTTCCTGTCGATCTGTAGGGACAGAGTCACCATCAC 62
QY 66 TTGACGGGCAAGTCAGGACATTAGTATTATTTAAATTTGGTATCAGGAAACACGAGAA 125
DB 63 TTGCGGGGCAAGTCAGGACATTAGTATTATTTAAATTTGGTATCAGGAAACACGAGAA 122
QY 126 AGCTCCTAAGCTCCGATCTATGTTTGCATCCAGTTTGCAAGTGGGTCCTCCATCAAGGTT 185
DB 123 AGCCCTAAGCTCCGATCTATGTTTGCATCCAGTTTGCAAGTGGGTCCTCCATCAAGGTT 182
QY 186 CAGCGGCAAGTGGATCTGGGACAGATTCACTCTCACCTCAGCAGCCTGCAGCCTGGAAGA 245
DB 183 CAGTGGCAAGTGGATCTGGGACAGATTCACTCTCACCTCAGCAGCCTGCAGCCTGGAAGA 242
QY 246 TTTTCGGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGAGGTTTCGGCCAGGGAC 305
DB 243 TTTTCGAACTTACTACTGTCAACAGATTACAGTACCCCTCGGAGGTTTCGGCCAGGGAC 302
QY 306 CAAGTGGAATCAAA 321
DB 303 CAAGTGGAATCAAA 318

RESULT 5
US-09-848-798-222
; Sequence 222, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 222
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-848-798-222

Query Match      84.0%; Score 269.6; DB 10; Length 321;
Best Local Similarity 90.8%; Pred. No. 5.1e-80;
Matches 287; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 6 CCAGATGACCCAGTCTCCATCTTCCTGTCGATCTGTAGGGACAGAGTCACCATCAC 65
DB 3 CGAGCTCACCCAGTCTCCATCTTCCTGTCGATCTGTAGGGACAGAGTCACCATCAC 62
QY 66 TTGACGGGCAAGTCAGGACATTAGTATTATTTAAATTTGGTATCAGGAAACACGAGAA 125
DB 63 TTGCGGGGCAAGTCAGGACATTAGTATTATTTAAATTTGGTATCAGGAAACACGAGAA 122
QY 126 AGCTCCTAAGCTCCGATCTATGTTTGCATCCAGTTTGCAAGTGGGTCCTCCATCAAGGTT 185
DB 123 AGCCCTAAGCTCCGATCTATGTTTGCATCCAGTTTGCAAGTGGGTCCTCCATCAAGGTT 182
QY 186 CAGCGGCAAGTGGATCTGGGACAGATTCACTCTCACCTCAGCAGCCTGCAGCCTGGAAGA 245
DB 183 CAGTGGCAAGTGGATCTGGGACAGATTCACTCTCACCTCAGCAGCCTGCAGCCTGGAAGA 242
QY 246 TTTTCGGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGAGGTTTCGGCCAGGGAC 305
DB 243 TTTTCGAACTTACTACTGTCAACAGATTACAGTACCCCTCGGAGGTTTCGGCCAGGGAC 302
QY 306 CAAGTGGAATCAAA 321
DB 303 CAAGTGGAATCAAA 318

RESULT 6
US-10-172-317-3
; Sequence 3, Application US/10172317
; Publication No. US20030091561A1
; GENERAL INFORMATION:
; APPLICANT: van de Winkel, Jan G.J.
; APPLICANT: van Dijk, Marcus A.
; APPLICANT: Halk, Edward
; APPLICANT: Gerritsen, Arnout F.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO
; TITLE OF INVENTION: EPIDERMAL GROWTH FACTOR RECEPTOR (EGFR)
; FILE REFERENCE: GMI-020
; CURRENT APPLICATION NUMBER: US/10/172,317
; CURRENT FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: US 60/298,172
; PRIOR FILING DATE: 2001-06-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-172-317-3

Query Match      83.6%; Score 268.2; DB 15; Length 321;
Best Local Similarity 89.7%; Pred. No. 1.5e-79;
Matches 288; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 1 GACATCCAGATGACCCAGTCTCCATCTTCCTGTCGATCTGTAGGGACAGAGTCACC 60
DB 1 GCCATCCAGTGTGACCCAGTCTCCATCTTCCTGTCGATCTGTAGGGACAGAGTCACC 60
QY 61 ATCACTTGCAGGCAAGTCAGGACATTAGGTATTATTTAAATTTGGTATCAGCAGAAACCA 120
DB 61 ATCACTTGCAGGCAAGTCAGGACATTAGGTATTATTTAAATTTGGTATCAGCAGAAACCA 120
QY 121 GGAAAGCTCCTAAGCTCCTGATCTATGTTGCAATCCAGTTTGGAAAGTGGGGTCCCATCA 180
DB 121 GGAAAGCTCCTAAGCTCCTGATCTATGATGCTCCAGTTTGGAAAGTGGGGTCCCATCA 180
QY 181 AGTTTCAGCGGCAAGTCAGGACAGATTCACTCTCACCTCAGCAGCCTGCAGCCT 240
DB 181 AGTTTCAGCGGCAAGTCAGGACAGATTCACTCTCACCTCAGCAGCCTGCAGCCT 240
QY 241 GAAGATTTTTCGACTTATTACTGTCTACAGTTTATAGTACCCCTCGAGTTTCGGGCAA 300
DB 241 GAAGATTTTTCGACTTATTACTGTCTACAGTTTATAGTACCCCTCGAGTTTCGGGCAA 300
QY 301 GGGACCAAGTGGAATCAAA 321
DB 301 GGGACCAAGTGGAATCAAA 321

RESULT 7
US-10-320-094-3
; Sequence 3, Application US/10320094
; Publication No. US20030194403A1
; GENERAL INFORMATION:
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DB 123 AGCCCTAAGCTCCTGATCTATGTCATCCAGTTTTCGAAAGTGGGGTCCCATCAAGTT 182
QY 186 CAGCGGCAAGTGGATCTGGGACAGAGTTCACTCTCACCTCAGCAGCCTGCAGCCTGAAGA 245
DB 183 CAGTGGCAAGTGGATCTGGGACAGAGTTCACTCTCACCTCAGCAGCCTGCAGCCTGAAGA 242
QY 246 TTTTCGCACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGAGGTTTCGGCCAGGGAC 305
DB 243 TTTTCGCACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGAGGTTTCGGCCAGGGAC 302
QY 306 CAAGTGGAATCAAA 321
DB 303 CAAGTGGAATCAAA 318

RESULT 6
US-10-172-317-3
; Sequence 3, Application US/10172317
; Publication No. US20030091561A1
; GENERAL INFORMATION:
; APPLICANT: van de Winkel, Jan G.J.
; APPLICANT: van Dijk, Marcus A.
; APPLICANT: Halk, Edward
; APPLICANT: Gerritsen, Arnout F.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO
; TITLE OF INVENTION: EPIDERMAL GROWTH FACTOR RECEPTOR (EGFR)
; FILE REFERENCE: GMI-020
; CURRENT APPLICATION NUMBER: US/10/172,317
; CURRENT FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: US 60/298,172
; PRIOR FILING DATE: 2001-06-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-172-317-3

Query Match      83.6%; Score 268.2; DB 15; Length 321;
Best Local Similarity 89.7%; Pred. No. 1.5e-79;
Matches 288; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 1 GACATCCAGATGACCCAGTCTCCATCTTCCTGTCGATCTGTAGGGACAGAGTCACC 60
DB 1 GCCATCCAGTGTGACCCAGTCTCCATCTTCCTGTCGATCTGTAGGGACAGAGTCACC 60
QY 61 ATCACTTGCAGGCAAGTCAGGACATTAGGTATTATTTAAATTTGGTATCAGCAGAAACCA 120
DB 61 ATCACTTGCAGGCAAGTCAGGACATTAGGTATTATTTAAATTTGGTATCAGCAGAAACCA 120
QY 121 GGAAAGCTCCTAAGCTCCTGATCTATGTTGCAATCCAGTTTGGAAAGTGGGGTCCCATCA 180
DB 121 GGAAAGCTCCTAAGCTCCTGATCTATGATGCTCCAGTTTGGAAAGTGGGGTCCCATCA 180
QY 181 AGTTTCAGCGGCAAGTCAGGACAGATTCACTCTCACCTCAGCAGCCTGCAGCCT 240
DB 181 AGTTTCAGCGGCAAGTCAGGACAGATTCACTCTCACCTCAGCAGCCTGCAGCCT 240
QY 241 GAAGATTTTTCGACTTATTACTGTCTACAGTTTATAGTACCCCTCGAGTTTCGGGCAA 300
DB 241 GAAGATTTTTCGACTTATTACTGTCTACAGTTTATAGTACCCCTCGAGTTTCGGGCAA 300
QY 301 GGGACCAAGTGGAATCAAA 321
DB 301 GGGACCAAGTGGAATCAAA 321

RESULT 7
US-10-320-094-3
; Sequence 3, Application US/10320094
; Publication No. US20030194403A1
; GENERAL INFORMATION:
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Db 121 GAGAAAGCCCTAAGTCCCTGATCTATGTCGATCCAGTTTGCAGAGTGGGGTCCCATCA 180
Qy 181 AGGTTTCAGGGCAGTGGATCTGGACAGAGTTTCACTCTCACCGTTCAGCAGCTTGCAGCCT 240
Db 181 AGGTTTCAGGGCAGTGGATCTGGACAGAGTTTCACTCTCACCGTTCAGCAGCTTGCAGCCT 240
Qy 241 GAAGATTTTGGACCTATTACTGTCTACAGTTTATAGTACCCCTCGAGTTTGGGCAA 300
Db 241 GAAGATTTTGGACCTATTACTGTCTACAGTTTATAGTACCCCTCGAGTTTGGGCAA 300
Qy 301 GGGACCAAGTGGAAATCAA 321
Db 301 GGGACCAAGTGGAAATCAA 321

RESULT 10
US-10-035-637-1
; Sequence 1, Application US/10035637
; Publication No. US20030031667A1
; GENERAL INFORMATION:
; APPLICANT: Deo, Yashwant M.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO DENDRITIC
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: MXI-166CP
; CURRENT APPLICATION NUMBER: US/10/035,637
; CURRENT FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 09/851,614
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/203,126
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: USSN 60/230,739
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(321)
US-10-035-637-1

Query Match 83.1%; Score 266.6; DB 15; Length 321;
Best Local Similarity 89.4%; Pred. No. 5.2e-79;
Matches 287; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Qy 1 GACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGCTGATCTGTAGGGGACAGATCACC 60
Db 1 GACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGCTGATCTGTAGGGGACAGATCACC 60
Qy 61 ATCATTGCGGGCAGTCCAGGATTTAGCAGGTTGGTATGTTTAAATTTGGTATCAGCAAAACA 120
Db 61 ATCATTGCGGGCAGTCCAGGATTTAGCAGGTTGGTATGTTTAAATTTGGTATCAGCAAAACA 120
Qy 121 GAAAAGTCTTAAAGTCTCTGATCTATGTTGATCCAGTTTGCAGTTGGGAGTGGGTTCCATCA 180
Db 121 GAAAAGTCTTAAAGTCTCTGATCTATGTTGATCCAGTTTGCAGTTGGGAGTGGGTTCCATCA 180
Qy 181 AGTTTCAGGGCAGTGGATCTGGACAGAGTTTCACTCTCACCGTTCAGCAGCTTGCAGCCT 240
Db 181 AGTTTCAGGGCAGTGGATCTGGACAGAGTTTCACTCTCACCGTTCAGCAGCTTGCAGCCT 240
Qy 241 GAAGATTTTGGACCTATTACTGTCTACAGTTTATAGTACCCCTCGAGTTTGGGCAA 300
Db 241 GAAGATTTTGGACCTATTACTGTCTACAGTTTATAGTACCCCTCGAGTTTGGGCAA 300
Qy 301 GGGACCAAGTGGAAATCAA 321
Db 301 GGGACCAAGTGGAAATCAA 321

RESULT 11
US-09-848-798-107
; Sequence 107, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-01-29
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 107
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 107
US-09-848-798-107

Query Match 83.0%; Score 266.4; DB 10; Length 321;
Best Local Similarity 90.2%; Pred. No. 6.1e-79;
Matches 285; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 6 CGAGATGACCCAGTCTCCATCTTCCCTGCTGCTGATCTGTAGGGGACAGATCACCATCAC 65
Db 3 CGAGTCAACCCAGTCTCCATCTTCCCTGCTGCTGATCTGTAGGGGACAGATCACCATCAC 62
Qy 66 TTGCGGGCAAGTCAGGACATAGGTATTTAAATTTGGTATCAGCAAAACCCAGGAA 125
Db 63 TTGCGGGCAAGTCAGGACATAGGTATTTAAATTTGGTATCAGCAAAACCCAGGAA 122
Qy 126 AGCTCTTAAGTCTCTGATCTATGTTGATCCAGTTTGCAGTTGGGTTCCATCAGGTT 185
Db 123 AGCCCTTAAGTCTCTGATCTATGTTGATCCAGTTTGCAGTTGGGTTCCATCAGGTT 182
Qy 186 CAGCGGCAAGTGGATCTGGGACAGATTTCACTCTCACCGTTCAGCAGCTTGCAGCTGAAGA 245
Db 183 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCGTTCAGCAGCTTGCAGCTGAAGA 242
Qy 246 TTTTGGCACTTATTAAGTCTCTGATCTATGTTGATCCAGTTTGCAGCTTGCAGCTTGCAGGAC 305
Db 243 TTTTGGCACTTATTAAGTCTCTGATCTATGTTGATCCAGTTTGCAGCTTGCAGCTTGCAGGAC 302
Qy 306 CAGGTGGAAATCAA 321
Db 303 CAGGTGGAAATCAA 318

RESULT 12
US-09-848-798-216
; Sequence 216, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-01-29
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 216

Query Match 82.6%; Score 265; DB 15; Length 321;
Best Local Similarity 89.1%; Pred. No. 1.8e-78;
Matches 286; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH47
US-09-848-798-216

Query Match 83.0%; Score 266.4; DB 10; Length 321;
Best Local Similarity 90.2%; Pred. No. 6.1e-79;
Matches 285; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH47
US-09-848-798-216

Query Match 82.5%; Score 264.8; DB 10; Length 321;
Best Local Similarity 89.9%; Pred. No. 2.1e-78;
Matches 284; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain P01
US-09-848-798-98

Query Match 82.6%; Score 265; DB 15; Length 321;
Best Local Similarity 89.1%; Pred. No. 1.8e-78;
Matches 286; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH47
US-09-848-798-216

Query Match 83.0%; Score 266.4; DB 10; Length 321;
Best Local Similarity 90.2%; Pred. No. 6.1e-79;
Matches 285; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH47
US-09-848-798-216

Query Match 82.5%; Score 264.8; DB 10; Length 321;
Best Local Similarity 89.9%; Pred. No. 2.1e-78;
Matches 284; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain P01
US-09-848-798-98

Search completed: June 19, 2004, 06:26:45
Job time : 286 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2004, 04:30:43 ; Search time 1734 Seconds
(without alignments)
5528.120 Million cell updates/sec

Title: US-09-019-441a-5_COPY_67_387

Perfect score: 321

Sequence: 1 gacatccagatgaccagtc.....gsaccaagtggaatacaaa 321

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 9921772

Minimum DB seq length: 0

Maximum DB seq length: 321

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estlin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_estc:*

9: gb_est1:*

10: gb_est2:*

11: gb_est3:*

12: gb_est4:*

13: gb_est5:*

14: gb_est6:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_pgk:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	223.6	69.7	269	10	AW404590 UI-HF-BL0
2	216.8	67.5	284	10	BF869849 IL3-ET011
3	213.4	66.5	270	10	AW406247 UI-HF-BL0
4	209.4	65.2	315	10	AW406545 UI-HF-BL0

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1

AW404590

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AW404590 269 bp cDNA linear EST 16-FEB-2000
UI-HF-BL0-acb-d-03-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3058588 5', mRNA sequence.

AW404590.1 GI:6923647

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 269)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: M.B. Soares Lab

cDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.lnl.gov/bbrp/image/image.html

Seq primer: M13 Forward.

ALIGNMENTS

AW404590 269 bp cDNA linear EST 16-FEB-2000
UI-HF-BL0-acb-d-03-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3058588 5', mRNA sequence.

AW404590.1 GI:6923647

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 269)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: M.B. Soares Lab

cDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.lnl.gov/bbrp/image/image.html

Seq primer: M13 Forward.


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www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3059828"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/lab_host="DH10B (LTI)"
/clone_lib="NIH_MGC_37"
/notes="Vector: p7773-Pac; Site 1: NotI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
ORIGIN
Query Match 66.5%; Score 213.4; DB 10; Length 270;
Best Local Similarity 88.2%; Pred. No. 4.7e-59; Indels 0; Gaps 0;
Matches 232; Conservative 0; Mismatches 31;
QY 7 CAGATGACCCAGTCTCCATCTTCCCTGCTGCACTGTAGGGGACAGAGTCAACCATCACT 66
Db 8 CAGATGACCCAGTCTCCATCTTCCCTGCTGCACTGTAGGGGACAGAGTCAACCATCACT 67
QY 67 TGCAGGGCAAGTCAGGACATTTAGGTATTTATTAATTTGGTATCAGAGAACCGAGAAA 126
Db 68 TGCATGCGAGTCAGGACATTTACCAACTATTTACATTTGGTATCATCAGAAACCGAGAAA 127
QY 127 GCTCTTAGCTCCTGATCTGTGTCATCTGCTGCACTGTAGGGGTCCTCCATCAAGGTTTC 186
Db 128 GCCCTTAGCTCCTGATCTAGTGCATCCATTTGGAAACAGGGTCCCATCAAGGTTTC 187
QY 187 AGCGGCACTGATCGGACAGAGTCACTCTACCGTCAGAGCCCTGACGCTGAGAT 246
Db 188 AGTGGAGTGCATCGGACAGAGATTTACTTTACCATCATGAGTCTGAGCTGAGAT 247
QY 247 TTGCGACTTATTACTGCTACA 269
Db 248 ATTGCAACATATTACTGCAACA 270
RESULT 4
AW406545 315 bp mRNA linear EST 16-FEB-2000
LOCUS
DEFINITION
IMAGE:3060199 5', mRNA sequence.
ACCESSION
AW406545
VERSION
AW406545.1 GI:6925602
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 315)
AUTHORS
NIH-MGC http://mgc.nci.nih.gov/
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
Location/Qualifiers
1. 254
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1. 315
/organism="Homo sapiens"
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/clone="IMAGE:3060199"
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/lab_host="DH10B (LTI)"
/clone_lib="NIH_MGC_37"
/notes="Vector: p7773-Pac; Site 1: NotI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
ORIGIN
Query Match 65.2%; Score 209.4; DB 10; Length 315;
Best Local Similarity 89.6%; Pred. No. 1.1e-57; Indels 0; Gaps 0;
Matches 225; Conservative 0; Mismatches 26;
QY 1 GACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGCACTGTAGGGGACAGAGTCAACC 60
Db 65 GACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGCACTGTAGGGGACAGAGTCAACC 124
QY 61 ATCACTTTCAGGGCAAGTCAGGACATTTAGGTATTTATTAATTTGGTATCAGCAGAACCA 120
Db 125 ATTACTTTCGGGCAAGTCAGTATTTAGTACTTATTTAAATTTGGTATCAGCAGAACCA 184
QY 121 GGAAGACCTCTTAAGCTCCTGATCTGTCATCTGTCAGATTTGCAAGTGGGTCCTCATCA 180
Db 185 GGGAGAGCCCTCCTAGGCTCCTGATCTATCTGCTTCCAGTTTGCAGATTTGCAAGTGGGTCCTCATCA 244
QY 181 AGGTTTCAGCGGCGAGTGGATCTGGGACAGAGTTCACCTCTCAACGTCAGAGCCCTGACGCT 240
Db 245 AGGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACTATCAACAGTCTGCAACCT 304
QY 241 GAAGATTTTGC 251
Db 305 GAAGATTTTGC 315
RESULT 5
AW406058 254 bp mRNA linear EST 16-FEB-2000
LOCUS
DEFINITION
IMAGE:3059040 5', mRNA sequence.
ACCESSION
AW406058
VERSION
AW406058.1 GI:6925150
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 254)
AUTHORS
NIH-MGC http://mgc.nci.nih.gov/
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
Location/Qualifiers
1. 254
/organism="Homo sapiens"
/mol_type="mRNA"
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Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN
Query Match 63.8%; Score 204.8; DB 10; Length 254;
Best Local Similarity 92.7%; Pred. No. 3.1e-56;
Matches 215; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1 GACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGCTATCTGAGGGGACAGAGTCAACC 60
DB 23 GACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGCTATCTGAGGGGACAGAGTCAACC 82

QY 61 ATCACTTTCAGGGCAAGTCAGGACATTAGGTATTATTAAATTCGTATCAGCAAAACCA 120
DB 83 ATCACTTTCAGGGCAAGTCAGGACATTAGGTATTAGGTATGATCAGCAAAACCA 142

QY 121 GGAAAGCTCTTACGCTCTGCTATCTGCTGCTATCTGCTGCTATCTGCTGCTATCTGCTGCT 180
DB 143 GGAAAGCTCTTACGCTCTGCTATCTGCTGCTATCTGCTGCTATCTGCTGCTATCTGCTGCT 202

QY 181 AGGTTTCAGGGCAAGTCAGGACATTAGGTATTATTAAATTCGTATCAGCAAAACCA 232
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RESULT 6
AA300891 303 bp mRNA linear EST 18-APR-1997
LOCUS EST14031 Testis tumor Homo sapiens cDNA 5' end similar to
DEFINITION immunoglobulin kappa light chain, V region, mRNA sequence.
ACCESSION AA300891
VERSION AA300891.1 GI:1953455
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 303)
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,
Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Uterback,T.R., Weidman,J.F., Li,Y.,
Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
Raymond,L., Wei,Y.P., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
Fraser,C.M. and Venter,J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
JOURNAL 96026280
MEDLINE 7566098
PUBMED
COMMENT Other_ESTs: THC167177
Contact: Kerlavage, AR
Bioinformatics

```

```

The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
Location/Qualifiers
1. 303
/organism="Homo sapiens"
/mol_type="mRNA"
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/dev_stage="adult"
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ORIGIN
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Best Local Similarity 91.1%; Pred. No. 7.3e-56;
Matches 214; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 2 ACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGCTATCTGAGGGGACAGAGTCAACC 61
DB 68 ACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGCTATCTGAGGGGACAGAGTCAACC 127

QY 62 TCATCTTTCAGGGCAAGTCAGGACATTAGGTATTATTAAATTCGTATCAGCAAAACCA 121
DB 128 TCATCTTTCAGGGCAAGTCAGGACATTAGGTATTATTAAATTCGTATCAGCAAAACCA 187

QY 122 GAAAGCTCTTACGCTCTGCTATCTGCTGCTATCTGCTGCTATCTGCTGCTATCTGCTGCT 181
DB 188 GAAAGCTCTTACGCTCTGCTATCTGCTGCTATCTGCTGCTATCTGCTGCTATCTGCTGCT 247

QY 182 GGTTCAGGGCAAGTCAGGACATTAGGTATTATTAAATTCGTATCAGCAAAACCA 236
DB 248 GGTTCAGGGCAAGTCAGGACATTAGGTATTATTAAATTCGTATCAGCAAAACCA 302

RESULT 7
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LOCUS EST13648 Testis tumor Homo sapiens cDNA 5' end similar to
DEFINITION immunoglobulin kappa light chain, V region, mRNA sequence.
ACCESSION AA300788
VERSION AA300788.1 GI:1953120
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 303)
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,
Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Uterback,T.R., Weidman,J.F., Li,Y.,
Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
Raymond,L., Wei,Y.P., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
Fraser,C.M. and Venter,J.C.

```

TITLE Initial assessment of human gene diversity and expression patterns
JOURNAL based upon 83 million nucleotides of cDNA sequence
MEDLINE Nature 377 (6547 Suppl), 3-174 (1995)
PUBMED 96026280
COMMENT 7566098
 Other ESTs: THC167177
 Contact: Kerlavage, AR
 Bioinformatics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699056
 Fax: 3018699423
 Email: arkerlav@igr.org

For clone availability, additional sequence and expression
 information related to this EST, please check the TIGR Human Gene
 Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
 Seq primer: M13 Reverse.
FEATURES
 Location/Qualifiers
 1..303
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 /mol_type="mRNA"
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 EcoRI; Site_2: XhoI"

FEATURES
 source

ORIGIN
 Query Match 63.4%; Score 203.6; DB 9; Length 303;
 Best Local Similarity 91.5%; Pred. No. 8.5e-56;
 Matches 215; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
 QY 2 ACATCCAGATGACCCAGTCTCCATCTCCCTCTGCTGCTAGGGACAGATCACC 61
 Db 69 ACATCCAGATGACCCAGTCTCCATCTCCCTCTGCTGCTAGGGACAGATCACC 128
 QY 62 TCACCTTGCGGCGAGTCAGACATAGTATATTTAAATTTGGTATCAGCAGAACCCAG 121
 Db 129 TCACCTTGCGGCGAGTCAGACATAGTATATTTAAATTTGGTATCAGCAGAACCCAG 188
 QY 122 GAAAGTCTTAACTCTGATCTATGTCATCAGTTTGCAGTGGGGTCCCATCA 181
 Db 189 GGAAGAGCCCTAATCTCTGATCTCTGCTGATCAGTTTGCAGTGGGGTCCCATCA 248
 QY 182 GGTTCAGGCGAGTGTGATCTGGACAGATTCACCTCTCAGCAGCCTGCA 236
 Db 249 GGTTCAGTGTGATGTGAGTCTGGACAGATTCACCTCTCAGCAGCCTGCA 303

RESULT 8
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LOCUS PM3-UT0058-060900-004-e03 UT0058 Homo sapiens cDNA, mRNA sequence.
DEFINITION BF095147
ACCESSION BF095147.1 GI:10900766
VERSION EST.
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 276)
AUTHORS Dias Neto,B., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
 O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
TITLE Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
JOURNAL 20202663
MEDLINE

PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the PAPSP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2-PM3-UT0058-060>)
 900-004-e03kt3=2000-09-06&t4=1
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 Site_2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

ORIGIN
 Query Match 62.3%; Score 200; DB 10; Length 276;
 Best Local Similarity 91.4%; Pred. No. 1.2e-54;
 Matches 234; Conservative 0; Mismatches 20; Indels 2; Gaps 2;
 QY 15 CCATCTCCATCTTCCCTGTCGATCTGTAGGGACAGATCACCATCATTTCAGGGC 74
 Db 22 CCAGTCTCCATCTTCCCTGTCG-ATCTGTAGGACAGATCACCATACTTCCCGGC 80
 QY 75 AAGTCAGACATTAGTATTATTAAATTTGGTATCAGCAGAAACAGGAAAGCTCTAA 134
 Db 81 AAGTCAGACATTAGCAGCTATTTAATTTGGTATCAGCAGAAACAGG-AAAGCCCCCTAA 139
 QY 135 GTCCTCATCTATGTCATCCAGTTTGCAGTGGGGTCCCATCAAGTTTCAGCGGAG 194
 Db 140 GTCCTCATCTATGTCATCCAGTTTGCAGTGGGGTCCCATCAAGTTTCAGTGGCAG 199
 QY 195 TGGATCTGGGACAGATTCCTCTCAGCAGCCTGCGAGCTTCAAGATTTTGGAC 254
 Db 200 TGGATCTGGGACAGATTCCTCTCAGCAGCCTGCGAGCTTCAAGATTTTGGAC 259
 QY 255 TTATTACTGTCTACAG 270
 Db 260 TTACTACTGTCAACAG 275

RESULT 9
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DEFINITION IMAGE:3061702 5', mRNA sequence.
ACCESSION AM407313
VERSION AM407313.1 GI:6926370
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 280)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cga@pe-rmail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward

FEATURES

Location/Qualifiers
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Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Query Match 61.9%; Score 198.8; DB 10; Length 280;
Best Local Similarity 85.7%; Pred. No. 3.1e-54;
Matches 221; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 1 GACATCAGATGACCCAGTCTCCATCTTCCTGTCGATCTGTAGGGGACAGATCAC 60
DB 23 GACATCAGATGACCCAGTCTCCATCTTCCTGTCGATCTGTAGGGGACAGATCAC 82
QY 61 ATCACTTGGCGGCAAGTCAGACATAGGTATTTAAATTTGGTATCAGCAACCA 120
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QY 121 GGAAGAGCTCTAAGCTCTGATCTATGTTGATCCAGTTTGCAAGTGGGGTCCCATCA 180
DB 143 GGGAAAGCCCCCTAAGCTCTGATCTATTAAGGCATCTAGTTTGAAGTAAAGTTCCATCA 202
QY 181 AGGTTACGCGCAGTGCATCTGGACAGATTCATCTCACCCTGACAGCCTGCAGCCT 240
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DB 263 GATGATTTCGACTTAT 280

RESULT 10

BF869187 304 bp mRNA linear EST 17-JAN-2001
LOCUS
DEFINITION IL3-ET0115-181000-294-F05 ET0115 Homo sapiens cDNA, mRNA sequence.

ACCESSION

BF869187

VERSION

BF869187.1 GI:12259317

KEYWORDS

EST

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 304)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brustein, A., de Oliveira, P.S., Sucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.

TITLE

Shotgun sequencing of the human transcriptome with ORF expressed

JOURNAL

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE

20202663

PubMed

10737800

COMMENT

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?i=IL3&t2=IL3-ET0115-
181000-294-F05&t3=2000-10-18&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 303.

FEATURES

source

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/dev_stage="Adult"
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/note="Organ: lung tumor; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Query Match 61.4%; Score 197.2; DB 10; Length 304;
Best Local Similarity 82.5%; Pred. No. 1.1e-53;
Matches 236; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

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DB 61 TTGCGGGGCAAGTCAGACATAGGTATTTAAATTTGGTATCAGCAACCAACGAGAG 120
QY 126 AGCTCTAGCTCTTCGATCTATGTTGATCCAGTTTGCAAGTGGGGTCCCATCAAGGTT 185
DB 121 AGCCCTAACTCTTAATCTACAGGGGCTCTACTTTAGAGAGTGGGGTCCCATCAAGGTT 180
QY 186 CAGCGGCGAGTGGATCTGGGACAGAGTTCATCTCACCCTGACAGCCTGCAGCCTGAGA 245
DB 181 CAGCGGCGAGTGGATCTGGGACAGAGTTCATCTCACCCTGACAGCCTGCAGCCTGATGA 240
QY 246 TTTTGGGACTTATTACTGTCACAGTTTATAGT 279
DB 241 TTTTGGGACTTATTCTTCCGACAGATCATATT 274

RESULT 11

AA377295

LOCUS

DEFINITION

Small intestine II Homo sapiens cDNA 5' end similar to

immunoglobulin kappa light chain, V region, mRNA sequence.

AA377295

ACCESSION

AA377295

VERSION

AA377295.1 GI:2029613

KEYWORDS

EST

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 301)

REFERENCE

AUTHORS

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,

TITLE	Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
JOURNAL	Nature 377 (6547 Suppl), 3-174 (1995)
MEDLINE	96026280
COMMENT	Other ESTs: EST89836 THC167177 75660398 Contact: Kerlavage, AR Bioinformatics The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 USA Tel: 3018699056 Fax: 3018699423 Email: akerlavet@tigr.org For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/db/hgi/hgi.html) Seq primer: M13 Reverse.

EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 283)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://bio-llnl.gov/bbrp/image/image.html>
Seq primer: M13 Forward.

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/note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5Kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN
Query Match 60.0%; Score 192.6; DB 10; Length 283;
Best Local Similarity 87.9%; Pred. No. 3.5e-52;
Matches 210; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
QY 45 AGGGAGCAGAGTCACCATCAGTTCGAGGGCAGTCAGGACATGATTAATTAATTC 104
DB 31 AGGAGCAGAGTCACCATCAGTTCGAGGGCAGTCAGGACATGATTAATTAATTC 90
QY 105 GTATCAGCAGAAACAGGAAAAGCTCCTAAGCTCCTGATCTATGTCATCCACAGTTTGA 164
DB 91 GTATCAGCAGAAACAGGAAAAGCTCCTGATCTATGTCATCCACAGTTTGA 150
QY 165 AAGTGGGGTCCCATCAAGGTTTCAGGGCAGTGGAGTCGGGACAGAGTTCTCTACCGT 224
DB 151 AAGTGGGGTCCCATCAAGGTTTCAGGGCAGAGGATCTGGGACAGATTTCAGTCTCACC 210
QY 225 CAGCAGCTGCGACCTGAGATTTCGCGATTTACTCTCTACAGITTTATAGTACCC 283
DB 211 CACAGTCTGCAACTGAGATTTCGCACTTACTCTCTACAGAGTTACATACCC 269

RESULT 13
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LOCUS BM856175
DEFINITION K-EST0139826 S14K402 Homo sapiens cDNA clone S14K402-53-D11 5',
mRNA sequence.
ACCESSION BM856175
VERSION BM856175.1 GI:19212574
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 321)
Kim.N.S., Hahn.Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,

Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.
 21C Frontier Korean EST Project 2001
 Unpublished (2002)
 CONTACT: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 53 row: D column: 11
 High quality sequence stop: 321.

FEATURES
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 Location/Qualifiers

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 /mol_type="mRNA"
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 /note="Organ: Stomach; Vector: pTZ19RP1; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then deapped with tabacco acid pyrophosphatase (TAP). The deapped intact mRNA was ligated with DNA-RNA linker including BcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 59.3%; Score 190.4; DB 12; Length 321;
 Best Local Similarity 88.8%; Pred. No. 2e-51;
 Matches 206; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1 GACATCCAGATGACCCAGTCCATCTTCCCTCTGCTGCTAGTGGGACAGAGTCACC 60
 DB 90 GACATCCAGATGACCCAGTCCATCTTCCCTCTGCTGCTAGTGGGACAGAGTCACC 149
 QY 61 ATCACTTGCAGGGCAAGTCCAGGACATTAGGTATTATTAAATTGGTATCAGCAAAACCA 120
 DB 150 ATCGTTGCCGGCAAGTCCAGGCGTCAGCAACTATTATTAAATTGGTATCAGCAAAACCA 209
 QY 121 GGAAGACTCTTAAGTCTTCGATCTATGTCATCCAGTTGCAAGTGGGTCACATCA 180
 DB 210 GGGAGAGCCCTAAGTCTTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCA 269
 QY 181 AGGTTTCAGGGCAGTGGATCTGGGACAGATTCACCTCACCCTCAGCAGCC 232
 DB 270 ATGTTTCAGTGGCAGTGGATCTGGGACAGATTCACCTCACCCTCAGCAGTC 321

RESULT 14
 CD686963
 LOCUS
 DEFINITION EST3494 human nasopharynx Homo sapiens cDNA, mRNA sequence.
 ACCESSION CD686963
 VERSION CD686963.1 GI:32204374
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 276)

AUTHORS
 TITLE
 JOURNAL
 COMMENT

Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and Zeng, Y.-X.
 Transcriptional Gene Expression Profile of Human Nasopharynx
 Unpublished (2003)
 CONTACT: Yixin Zeng
 Cancer Center
 Sun Yat-sen University
 651 Dongfeng Road East, Guangzhou 510060, China
 Tel: 86-1380-9770-743
 Fax: 86-20-8775-4506
 Email: yxzeng@gzsums.edu.cn.

FEATURES
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 1. 276
 Location/Qualifiers

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue="normal nasopharynx"
 /clone_lib="human nasopharynx"
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ORIGIN

Query Match 59.3%; Score 190.2; DB 14; Length 276;
 Best Local Similarity 89.9%; Pred. No. 2.1e-51;
 Matches 204; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

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 DB 110 ATCACTTGCAGGGCAAGTCCAGGACATTAGGTATTATTAAATTGGTATCAGCAAAACCA 169
 QY 121 GGAAGACTCTTAAGTCTTCTGATCTATGTCATCCAGTTGCAAGTGGGTCACATCA 180
 DB 170 GTGAAAGCCCTAAGTCCCTGATCTATGCTGCTATCTATGCTGCTATCTATCTATCA 229
 QY 181 AGGTTTCAGGGCAGTGGATCTGGGACAGATTCACCTCACCCTCAG 227
 DB 230 AAGTTTCAGGGCAGTGGATCTGGGACAGATTCACCTCACCCTCAG 276

RESULT 15
 AW407923
 LOCUS

DEFINITION UI-HP-B10-add-c-07-0-UI.r2 NIH_MGC_37 Homo sapiens cDNA clone
 IMAGE:3061236 5', mRNA sequence.

ACCESSION AW407923
 VERSION AW407923.1 GI:6926980
 KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Eco RI site shown at the beginning of the sequence.
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: M.B. Soares Lab
 cDNA Library Arrayed by: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html

FEATURES
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 1. 252
 Location/Qualifiers

/organism="Homo sapiens"

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2004, 07:32:38 ; Search time 1845 Seconds
(without alignments)
8316.224 Million cell updates/sec

Title: US-09-019-441A-7_COPY_58_411

Perfect score: 354

Sequence: 1 gaggtgcagtggtgagtc.....tctgtcaccgtctctctca 354

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 3056378

Minimum DB seq length: 0

Maximum DB seq length: 354

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_on.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_on.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_rod.*

36: em_htg_mam.*

37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	249.4	70.5	348	9 AF471251	AF471251 Homo sapi
2	246.4	69.6	348	9 AB063673	AB063673 Homo sapi
3	245.6	69.4	348	9 U00491	U00491 Human immun
4	242.4	68.5	348	9 AF231396	AF231396 Homo sapi
5	240.8	68.0	348	9 AB021526	AB021526 Homo sapi
6	240.8	68.0	348	9 HSIHAD13	X98751 H.sapiens m
7	239.2	67.6	348	9 HS080150	U00150 Human immun
8	238.8	67.5	342	9 AB066982	AB066982 Homo sapi
9	238.6	67.4	342	9 HSHV3183	X62972 H.sapiens r
10	237.6	67.1	345	9 HSU80154	U00154 Human immun
11	237.4	67.1	348	6 AX112674	AX112674 Sequence
12	236.6	66.8	351	6 AX474084	AX474084 Sequence
13	235.2	66.7	354	9 AF231402	AF231402 Homo sapi
14	235.2	66.4	348	9 AB063899	AB063899 Homo sapi
15	235.2	66.4	351	9 AB066979	AB066979 Homo sapi
16	234.4	66.2	345	9 AF471477	AF471477 Homo sapi
17	234.4	66.2	348	9 AF471559	AF471559 Homo sapi
18	234.4	66.2	348	9 AF471587	AF471587 Homo sapi
19	234.4	66.2	348	9 HSA556719	AJ556719 Homo sapi
20	233.6	66.0	348	6 AX112744	AX112744 Sequence
21	233.6	66.0	354	9 AB063699	AB063699 Homo sapi
22	233.4	65.9	348	9 AF471241	AF471241 Homo sapi
23	233.4	65.9	354	9 AF471245	AF471245 Homo sapi
24	232.8	65.8	346	9 AY055481	AY055481 Homo sapi
25	232.8	65.8	348	6 AX112640	AX112640 Sequence
26	232.8	65.8	348	9 HSA238037	AJ238037 Homo sapi
27	232.8	65.8	354	9 AF398962	AF398962 Homo sapi
28	232.6	65.7	351	9 AF004324	AF004324 Homo sapi
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30	231.6	65.4	333	9 AF174100	AF174100 Homo sapi
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32	231.2	65.3	345	9 HSA410905	AJ410905 Homo sapi
33	231.2	65.3	348	9 HSA556718	AJ556718 Homo sapi
34	230.4	65.1	349	6 AX112726	AX112726 Sequence
35	230.2	65.0	351	9 AB066881	AB066881 Homo sapi
36	230.2	65.0	335	9 AF174105	AF174105 Homo sapi
37	229.6	64.9	348	12 AY180097	AY180097 Synthetic
38	229.6	64.9	349	9 HOMVH3S	D83693 Human mRNA
39	229.6	64.9	354	9 AF455546	AF455546 Homo sapi
40	228.6	64.6	351	6 AX339676	AX339676 Sequence
41	228.6	64.4	348	9 AF471377	AF471377 Homo sapi
42	228.6	64.4	354	9 HSA298611	AJ298611 Homo sapi
43	227.8	64.4	342	9 HSHV3RGLA	X70468 H.sapiens D
44	227.2	64.2	339	9 HSHCV03	X99354 H.sapiens m
45	227.2	64.2	345	9 AB063896	AB063896 Homo sapi

ALIGNMENTS

RESULT 1	AF471251	348 bp	mRNA	linear	PRI 11-OCT-2003
LOCUS	Homo sapiens clone 56-58a Ig heavy chain variable region, VH3				
DEFINITION	Family mRNA, partial cds.				
ACCESSION	AF471251				
VERSION	AF471251.1	GI:33319045			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 348)				
AUTHORS	Scamurri,R.W., Nelson,D.B., Miller,D.J., Lorenz,E. and Janoff,E.N.				
TITLE	Impact of HIV-1 on Somatic Hypermutation in Mucosal B Cells				

Pred. No. is the number of results predicted by chance to have a

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 348)
AUTHORS Scamurra,R.W., Nelson,D.B., Miller,D.J., Lorenz,E. and Janoff,E.N.
TITLE Direct Submission
JOURNAL Submitted (22-JAN-2002) Division of Infectious Diseases- 111F,
Mucosal and Vaccine Research Center, Veterans Affairs Medical
Center, One Veterans Drive, Minneapolis, MN 55417, USA
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Best Local Similarity 83.9%; Pred. No. 3.4e-56;
Matches 296; Conservative 0; Mismatches 51; Indels 6; Gaps 1;
Qy 2 AGTGCAGCTGTGGAGCTCTGGGGCGGCTTGGCAAGCTGGGGGTCCTCGAGACTCT 61
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Qy 62 CCTGGCAGCTCCGGGTTTCAGGTTTCACCTTCAATACCTACTACATGAGTGGTCCGCC 121
Db 62 CCTGTGAGCTCTG-----GATTCACCTTCAGTCTACTACATGAGTGGTCCGCC 115
Qy 122 AGGCTCCAGGCGAGGGCTGGAGTGGGCTCTCAGCTATTAGTAGTGGTGGTCCACAT 181
Db 116 AGGCTCCAGGCGAGGGCTGGAGTGGGCTTTTATACATTAGTAGTGGTGGTACCATAT 175
Qy 182 GGTACGAGACTCCGTGAAGGCGGATTCACCTCCAGAGAGAGCCCAACACAC 241
Db 176 TCTACGAGACTCTGTGAAGGCGGATTCACCTCCAGGAGACAGCCCAAGACTCAC 235
Qy 242 TGTTTCTTCAAAATGAACAGAGCTGAGAGCTGAGGACAGCGGCTGTCTATTACTGTGCGAGCT 301
Db 236 TGTATCTGCAATGAACAGAGCTGAGAGCCGAGGACAGCGGCTGTATTACTGTGCGAGAG 295
Qy 302 TGACTACAGGCTCTGACTCTGGGCGCAGGAGTCTGTGTCACGGTCTCTCA 354
Db 296 CAAGCCCTACTTTGACTACTGTGGCGCAGGGAACCCCTGGTCCACCGTCTCTCA 348
RESULT 2
LOCUS AB063673 348 bp mRNA linear PRI 02-JUL-2002
DEFINITION Homo sapiens IGH mRNA for immunoglobulin heavy chain VHJ region,
partial cds, clone:JH23.
ACCESSION AB063673
VERSION AB063673.1 GI:21668547
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1
Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M.,
Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J.,
Miura,K. and Kurosawa,Y.
TITLE Construction and characterization of antibody libraries: isolation
of therapeutic human antibodies and application to functional
genetics
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 348)
AUTHORS Kurosawa,Y.
TITLE Direct Submission
JOURNAL Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
Comprehensive Medical Science, Fujita Health University,
Kutsukake-cho, Toyosake 470-1192, Japan
(E-mail:kurosawa@fujita-hu.ac.jp, tel:81-562-93-9387)
Please visit our web site
URL:http://www.fujita-hu.ac.jp/immunity/
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Best Local Similarity 83.7%; Pred. No. 2.1e-55;
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Qy 121 CAGGCTCCAGGCGAGGGCTGGAGTGGGCTCTCAGCTATTAGTAGTGGTGGTATCCACA 180
Db 115 CAGGCTCCAGGCGAGGGCTGGAGTGGGCTTTCATACATTAGTAGTGGTGGTATCCATA 174
Qy 181 TGGTACGAGACTCCGTGAAGGCGAGATTTCACCTCTCCAGAGAGAACCCCAACACACA 240
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Qy 241 CTGTTTCTTCAAAATGAACAGAGCTGAGAGCTGAGGACAGCGGCTGTCTATTACTGTGCGAGC 300
Db 235 CTGTATCTGCAAAATGAACAGAGCTGAGAGCCGAGGACAGCGGCTGTATTACTGTGCGAGA 294
Qy 301 TTGACTACAGGCTCTGACTCTCTGGGCGCAGGAGTCTCTGGTCCACCGTCTC 350
Db 295 GGTGGGGAACCTTGTACTACTGGGCGCAGGGAACCCCTGGTCCACCGTCTC 344
RESULT 3
LOCUS U00491 348 bp mRNA linear PRI 08-MAY-1994
DEFINITION Human immunoglobulin heavy chain variable region (clone Amuic3-3)

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mRNA, partial cds.
ACCESSION U00491
VERSION U00491.1 GI:392577
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 348)
AUTHORS Huang, C. and Stollar, B.D.
TITLE A majority of Ig H chain cDNA of normal human adult blood
JOURNAL lymphocytes resembles cDNA for fetal Ig and natural autoantibodies
MEDLINE J. Immunol. 151 (10), 5290-5300 (1993)
PUBMED 94044753
2282225
REFERENCE 2 (bases 1 to 348)
AUTHORS Stollar, B.D.
TITLE Direct Submission
JOURNAL Submitted (10-AUG-1993) Stollar B.D., Tufts University,
Biochemistry, 136 Harrison Ave., Boston, MA 02111, USA
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Best Local Similarity 83.1%; Pred. No. 3.5e-55;
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QY 61 TCCTGCGCAGCTCCGGGTTCCAGTTTCACCTTCATTAACCTACTACATGAGCTGGGTCCGC 120
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LOCUS
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Homo sapiens clone 1-3 immunoglobulin heavy chain variable region
mRNA, partial cds.
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VERSION AF231396.1 GI:8489278
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 348)
AUTHORS Glas, A.M., van Montfort, B.H.N., Storek, J., Green, E.N., and
Drissen, R.P., Bechtold, V.J., Reilly, J.Z., Dawson, M.A., and
Milner, E.C.B.
TITLE B cell-autonomous somatic mutation deficit following bone marrow
transplant
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 348)
AUTHORS Glas, A.M. and Milner, E.C.B.
TITLE Direct Submission
JOURNAL Submitted (07-FEB-2000) Virginia Mason Research Institute, 1201 9th
Ave, Seattle, WA 98101, USA
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DB 1 GAGGTGACGCTGGTGGAGTCTGGGGCGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTC 60
QY 61 TCCTGCGCAGCTCCGGGTTCCAGTTTCACCTTCATTAACCTACTACATGAGCTGGGTCCGC 120
DB 61 TCCTGCGCAGCTCTG-----GATTACCTTTAGCAGCTATGCCATGAGCTGGGTCCGC 114
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QY 181 TGGTAGCGAGCTCCGTGAAGGCGAGATTACCATCTCCAGAGAGAACCCCAACACACA 240
DB 175 TACTACGCGAGCTCCGTGAAGGCGCGGTTCCACCATCTCCAGAGACAAATCCAGAACACG 234
QY 241 CTGTTTCTTCAATGAACAGCTGAGAGCTGAGGACACCGGCTGTCTATTACTGTGCGAGC 300
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QY 301 TTGACTACAGGGTCTGACTCTCTGGGGCCAGGGAGTCCCTGTCACCGTCTCTCTCA 354
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RESULT 5
AS021526
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LOCUS AB021526 348 bp mRNA linear PRI 27-MAR-2002
DEFINITION Homo sapiens mRNA for immunoglobulin heavy chain variable region (IGH), partial cds, clone krpbc21.
ACCESSION AB021526
VERSION AB021526.1 GI:4107065
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 Hakoda M., Taniguchi, A., Kotake, S., Higami, K., Ichikawa, N., Silverman, G.J. and Kamatani, N.
TITLE Pathogenic implication of a prototype B cell superantigen, staphylococcal protein A, in rheumatoid arthritis
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 348)
AUTHORS Hakoda, M.
TITLE Direct Submission
JOURNAL Submitted (18-DEC-1998) Masayuki Hakoda, Tokyo Women's Medical University, Institute of Rheumatology; 10-22 Kawada-cho Shinjuku-ku, Tokyo 162-0054, Japan
KEYWORDS (E-mail: ratoriyomomo.so-net.or.jp, Tel:81-3-5269-1725, Fax:81-3-5269-1726)
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QY 301 TTGACTACAGGGTCTGATCTCTGGGGCCAGGGAGTCTCTGGTCAACCGTCTCTCA 354
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DEFINITION X98751
ACCESSION X98751.1 GI:1430804
VERSION X98751.1
KEYWORDS heavy chain; immunoglobulin; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 Dorsam, H., Kipriyanov, S., Welschhof, M. and Little, M.
TITLE Isolation of an anti-Digoxigenin antibody out of an human IGM-Antibody library and expression in E.coli
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 348)
AUTHORS Dorsam, H.
TITLE Direct Submission
JOURNAL Submitted (24-JUN-1996) H. Dorsam, German Cancer Research Center, Diagnostics and Experimental Therapy Program, Recombinant Antibody Group, INF 280, 69120 Heidelberg, FRG
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Qy	181	TGGTAGCAGACTCGTGAAGGAGATTCACCATCTCCAGAGAGAACCCAAACACACA	240
Db	175	TACTAGCAGACTCGTGAAGGAGGCGGTTCACCTCTCCAGAGACAAATCCAGAGACAG	234
Qy	241	CTGTTTCTTCAATGAACAGCCTGAGAGCTGAGAGACAGCGGCTGTCTATTACTGTGCGAGC	300
Db	235	CTGTATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCGGTATATTACTGTGCGAAA	294
Qy	301	TTGACTACAGGTCTGACTCTCGGGGCCAGGAGTCCCTGGTCAACCGTCTCTCTCA	354
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DEFINITION	Human immunoglobulin heavy chain variable region (V3-23) gene, partial cds.		
ACCESSION	U80150		
VERSION	U80150.1	GI:1791142	
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Homo sapiens (human)		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Glas,A.M., Nottenburg,C. and Milner,E.C.		
TITLE	Analysis of rearranged immunoglobulin heavy chain variable region genes obtained from a bone marrow transplant (BMT) recipient		
JOURNAL	Clin. Exp. Immunol. 107 (2), 372-380 (1997)		
MEDLINE	97182739		
PUBMED	9030878		
REFERENCE	2 (bases 1 to 348)		
AUTHORS	Glas,A.M., Nottenburg,C. and Milner,E.C.B.		
TITLE	Direct Submission		
JOURNAL	Submitted (29-NOV-1996) Immunology, Virginia Mason Research Center, 1000 Seneca Street, Seattle, WA 98101, USA		
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Best Local Similarity	81.9%; Pred. No. 1.8e-53;		
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Qy	61	TCCTGCGCAGCCTCCGGGTTTCAGGTTTCAATTAACCTACTACATGGACTGGGTCCGC	120
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Qy	121	CAGGCTCCAGGAGAGGGGCTGGAGTGGGTCTCAGCTATTAGTAGTACTGTGATCCCA	180
Db	115	CAGGCTCCAGGAGAGGGGCTGGAGTGGGTCTCAGCTATTAGTAGTACTGTGATCCCA	174
Qy	181	TGTTACGACAGACTCCGTGAAGGSCAGATTCCACCATCTCCAGAGAGAACGCCAACACA	240
Db	175	TACTACGACAGACTCCGTGAAGGSCGCTTCAACCATCTCCAGAGACAATCCAGAACAG	234
Qy	241	CTGTTTCTTCAATGAACAGCCTGAGAGCTGAGGACAGCGCTGTCTATTACTGTGCGAGC	300
Db	235	CTGTATCTGCAAAATGAACAGCCTGAGAGCCGAGGACACGGCGGTATATTACTGTGCGAAA	294
Qy	301	TTGACTACAGGTCTGACTCTCTGGGGCCAGGAGTCCCTGGTCAACCGTCTCTCTCA	354
Db	295	GATCGGTATAGCAGCTCGTCTCTGGGGCCAGGAAACCTGGTCAACCGTCTCTCTCA	348
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DEFINITION	Homo sapiens IGH mRNA for immunoglobulin heavy chain VHDJ region, partial cds, clone:aims0023h.		
ACCESSION	AB066982		
VERSION	AB066982.1	GI:21670020	
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M., Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J., Miura,K. and Kurosawa,Y.		
TITLE	Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional genomics		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 342)		
AUTHORS	Kurosawa,Y.		
TITLE	Direct Submission		
JOURNAL	Submitted (25-JUL-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University, Immunology; Kutsukake-cho, Toyoake, Aichi 470-1192, Japan (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)		
COMMENT	Please visit our web site		
FEATURES	URL:http://www.fujita-hu.ac.jp/immunity/.		
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ORIGIN
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Best Local Similarity 83.6%; Pred. No. 5e-53;
Matches 296; Conservative 0; Mismatches 49; Indels 9; Gaps 2;

QY 1 GAGGTGACGCTGGTGGAGTCTGGGGCGGCTGGGCAAGCCCTGGGGGGTCCCTGAGACTC 60
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Best Local Similarity 83.6%; Pred. No. 9.2e-53;
Matches 295; Conservative 0; Mismatches 49; Indels 9; Gaps 2;

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DB 61 TCCTGCGCAGCCTCTG-----GATTCACCTTCACTACTACTAGCTGGATCCGC 114

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QY 115 CAGGCTCCAGGGCAGGGCTGGAGTGGGTCTCACGTTATTAGTAGTGGTATCCCA 174
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QY 235 CTGTATCTGCAAAATGAACAGCCTGAGAGCCGAGGACACCGGCTGTCTATTACTGTGCGAGA 294
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Best Local Similarity 83.6%; Pred. No. 9.2e-53;
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DEFINITION
Sequence 155 from Patent WO0127279.
ACCESSION
AX112674
VERSION
AX112674.1 GI:13939321
KEYWORDS
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Edwards,B.M., Main,S.H. and Vaughan,T.J.
TITLE
Human anti-adipocyte monoclonal antibodies and their use
JOURNAL
Patent: WO 0127279-A 155 19-APR-2001;
Cambridge Antibody Technology (GB)
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Best Local Similarity 82.2%; Pred. No. 5.6e-53;
Matches 287; Conservative 0; Mismatches 56; Indels 6; Gaps 1;

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QY 62 CCGCGCAGCCTCCGGGTTTCAGGTTTCACCTTCAATPACTACTACATGGAGTGGGTCCGC 121
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LOCUS      Homo sapiens clone 4-4 immunoglobulin heavy chain variable region
DEFINITION      mRNA, partial cds.
ACCESSION      AF231402
VERSION      AF231402.1 GI:8489289
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 354)
AUTHORS      Glas, A.M., van Montfort, E.H.N., Storek, J., Green, E.N., and
Drissen, R.P., Bechtold, V.J., Reilly, J.Z., Dawson, M.A., and
Milner, E.C.B.
TITLE      B cell-autonomous somatic mutation deficit following bone marrow
transplant
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 354)
AUTHORS      Glas, A.M. and Milner, E.C.B.
TITLE      Direct Submission
JOURNAL      Submitted (07-FEB-2000) Virginia Mason Research Institute, 1201 9th
Ave, Seattle, WA 98101, USA
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DB      235 CTGTATCTGCAATGAACAGCTGAGAGCCGAGGACAGCGCGGTATATTACTGTGCGAGG 294
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LOCUS      Homo sapiens IGH mRNA for immunoglobulin heavy chain VHDJ region,
DEFINITION      partial cds, clone:H249.
ACCESSION      AB063899
VERSION      AB063899.1 GI:21668999
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS      Akahori, Y., Iba, Y., Morino, K., Shinohara, M., Hirono, Y., Kakita, M.,
Suzuki, K., Torii, H., Ukai, Y., Honda, T., Katsumi, H., Okada, J.,
Miura, K. and Kurosawa, Y.
TITLE      Construction and characterization of antibody libraries: isolation
of therapeutic human antibodies and application to functional
genomics
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 348)
AUTHORS      Kurosawa, Y.
TITLE      Direct Submission
JOURNAL      Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
Comprehensive Medical Science, Fujita Health University;
Kutsukake-cho, Toyooka 470-1192, Japan
(S-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
Please visit our web site
URL:http://www.fujita-hu.ac.jp/immunity/.
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FDYWGQGTLVTVSS"
ORIGIN
Query Match      66.4%; Score 235.2; DB 9; Length 348;
Best Local Similarity 81.7%; Pred. No. 2.2e-52;
Matches 286; Conservative 0; Mismatches 58; Indels 6; Gaps 1;
QY      1 GAGGTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCCTGGGGGTCCTGAGACTC 60
DB      1 GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGTCCTGAGACTC 60
QY      61 TCCTGCGCAGCTCCGGGTTCAAGTTTCACTTCAATAACTACTACATGAGCTGGTCCGC 120
DB      61 TCCTGTTTCAAGCCTCTG-----GATTCACCTTCACTAGTATGCTATGCTGGTCCGC 114
QY      121 CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCAGTATTAGTAGTAGTGGTATCCCA 180
DB      115 CAGGCTCCAGGAAGGAGCTGGAATATGTTTCAGCTATTAGTAGTAGTGGGGTAGCACA 174
QY      181 TGGTAGCAGACTCCGTTGAAGGCGCAGATTCAACATCTCCAGAGAGAACGCCAACACACA 240
DB      175 TACTACGAGACTCCGTTGAAGGCGCAGATTCAACATCTCCAGAGAGAACATTCCAAAGAACAG 234
QY      241 CTGTTTCTTCAATGAACAGCTGAGAGCTGAGGACAGCGCTGTCTATTACTGTGCGAGC 300
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Db 235 CTGTATCTTCAATGAGAGCTGTGAGAGCTGAGACACGGCTGTGTATTACTGTGTGAA 294

Qy 301 TTGACTACAGGGTCTGACTCCTCGGGGCGAGGAGTCTCGTCAACCGTCTC 350

Db 295 AGTCGGGGTTCTTTGACTACTAGGGGCCAGGGAACCCCTGGTCAACCGTCTC 344

RESULT 15

AB066979

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Homo sapiens

REFERENCE

AUTHORS

1 Akahori, Y., Iba, Y., Morino, K., Shinohara, M., Hirono, Y., Kakita, M., Suzuki, K., Torii, H., Ukai, Y., Honda, T., Katsumi, H., Okada, J., Miura, K. and Kurosawa, Y.

TITLE

Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional genomics

JOURNAL

REFERENCE

2 (bases 1 to 351)

AUTHORS

Kurosawa, Y.

TITLE

Direct Submission

JOURNAL

Submitted (25-JUL-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University, Immunology, Kutsukake-cho, Toyosake, Aichi 470-1192, Japan (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)

COMMENT

Please visit our web site

URL: <http://www.fujita-hu.ac.jp/immunity/>.

FEATURES

source

1..351

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="aims0017h"

/clone_lib="AIMS4"

/note="mixture of tissues: tonsils, umbilical cords, peripheral blood and bone marrow"

1..351

/gene="IGH"

<1..>351

/gene="IGH"

/codon_start=1

/product="immunoglobulin heavy chain VHDJ region"

/protein_id="BAC02017.1"

/db_xref="GI:21670015"

/translation="EVQLVESGGGVQPGQSLRLCAASGFTPSYSMMNWVQAQPKG LEWVSSTSSSSSYIYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYICARDIAA AGNFWGQGTLVTVSS"

ORIGIN

Query Match 66.4%; Score 235; DB 9; Length 351;

Best Local Similarity 83.3%; Pred. No. 2.5e-52;

Matches 294; Conservative 0; Mismatches 50; Indels 9; Gaps 2;

Qy 1 GAGGTGAGCTGGTGGAGTCTGGGGGGCGCTTGCGAAGCGCTGGGGGTCCTCGAGACTC 60

Db 1 GAGGTACAGCTGGTGGAGTCTGGGGGAGGGGTGGTCCAGCTGGGAGTCCCTGAGACTC 60

Qy 61 TCCTGGCGAGCCTCCGGGTTTCAGGTTCACTTCAATTAATCTACTACATGGACTGGTCCGC 120

Db 61 TCCTGTGAGCCTCTG-----GATTCACCTTCAGTAGCTATAGCATGAACCTGGTCCGC 114

Qy 121 CAGCTCCAGCGGAGGGGCTGGAGTGGTCTCAGGTATTAGTAGTGTGATCCACACA 180

Db 115 CAGGCTCCAGGAGAGGGGCTGGAGTGGGTCTCATCCATTAGTAGTAGTTACATA 174

181 TGGTACGCAGACTCGGTGAAGGGCAGATTACCATCTCCAGAGAGAACGCCAACACACA 240

175 TACTACGCAGACTCAGTGAAGGGCCGATTACCATCTCCAGAGACACGCCAAGAACTCA 234

241 CTGTTTCTTCAAAATGAACAGCCTGAGAGCTGAGGACACAGGCTGTCTATTACTGTGGAGC 300

235 CTGTATCTGCAAAATGAACAGCCTGAGAGCCGAGGACACCGGCTGTGTATTACTGTGCGAGA 294

301 TTGACTACAGGGTCTG---ACTCTGTGGGGCCAGGGAGTCTCTGGTCAACCGTCTC 350

295 GATATAGCAGCAGCTGGTAACTACTTGGGGCCAGGGAACCCCTGGTCAACCGTCTC 347

Search completed: June 19, 2004, 08:52:20

Job time : 1848 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2004, 07:31:37 ; Search time 280 Seconds
(without alignments)
5370.936 Million cell updates/sec

Title: US-09-019-441A-7_COPY_58_411

Perfect score: 354

Sequence: 1 gaggtgcagctggggagtc.....tcctggtcacgcgtctctca 354

Scoring table: IDENTITY NUC

Gapop 10.0 ; Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 4221282

Minimum DB seq length: 0
Maximum DB seq length: 354

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_29Jan04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002s:*
7: Geneseqn2003as:*
8: Geneseqn2003bs:*
9: Geneseqn2003cs:*
10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	247.2	69.8	348	6 AAL39119	Antibody
2	241.6	68.2	348	6 AAD46290	Human KDR
3	241.6	68.2	348	7 ABT23325	VEGF bind
4	241.6	68.2	348	9 ADD24416	Human hea
5	241.6	68.2	348	9 ADD80793	Human cto
6	240	67.8	348	6 AAD46292	Human KDR
7	240	67.8	348	7 ABT23327	VEGF bind
8	240	67.8	348	9 ADD24420	Human hea
9	240	67.8	348	9 ADD80797	Human cto
10	238.4	67.3	348	6 AAD46294	Human KDR
11	238.4	67.3	348	7 ABT23329	VEGF bind
12	238.4	67.3	348	9 ADD24423	Human hea
13	238.4	67.3	348	9 ADD80800	Human cto
14	237.4	67.1	348	4 AAS03478	DNA encod
15	236.6	66.8	351	6 AAL43586	Dig3 anti
16	233.6	66.0	348	4 AAS03513	DNA encod
17	232.8	65.8	348	4 AAS03461	DNA encod
18	232.6	65.7	351	6 ABK90972	Human ant
19	230.4	65.1	349	4 AAS03504	DNA encod
20	228.6	64.6	351	6 ABA92717	Fibronect
21	226.4	64.0	354	4 AAS03470	DNA encod
22	223.8	63.2	354	2 AAT72127	CEA-speci
23	223.2	63.1	354	2 AAT72128	CEA-speci

24	223	63.0	348	4 AAS03445	DNA encod
25	222.6	62.9	294	7 ACC00475	Human ger
26	222.6	62.9	311	4 ABS46318	Human liv
27	222.6	62.9	311	6 ABS20923	Human gen
28	222.4	62.8	348	2 AAT72130	CEA-speci
29	222.4	62.8	354	4 AAH47513	Anti-IL-1
30	221.6	62.6	294	3 AAZ46860	Human imm
31	221.6	62.6	296	6 ABS62711	Germline
32	221.6	62.6	345	4 AAS03511	DNA encod
33	221	62.4	294	7 ACC00478	Human ger
34	220.4	62.3	339	3 AAZ27658	DNA encod
35	219	61.9	348	6 ABA94334	MAB 27A1
36	219	61.9	354	3 AAC96948	Human ant
37	218.4	61.7	345	6 ABA94332	MAB 12B5
38	218.2	61.5	351	6 ABA94338	MAB 63 he
39	217.8	61.5	294	3 AAZ46861	Human imm
40	217.4	61.4	336	3 AAZ27662	DNA encod
41	216.8	61.2	296	6 ABS62712	Germline
42	215.8	61.0	354	7 AAD45588	Human VEG
43	215.6	60.9	351	6 ABK88457	Human ant
44	215.4	60.8	351	2 AAQ64850	SpA-react
45	214.4	60.6	342	4 AAF29060	Human HIV

ALIGNMENTS

RESULT 1
AAL39119
ID AAL39119 standard; DNA; 348 BP.
AC AAL39119;
XX
DT 02-SEP-2002 (first entry)
XX
DE Antibody screening method related DNA VH(DP-47).
XX
KW Screening antibody; 2-D electrophoresis; plural protein; protein spot;
KW antibody library; proteomics; ds.
XX
OS Unidentified.
XX
PN WO200242774-A1.
XX
PD 30-MAY-2002.
XX
PF 05-JUN-2001; 2001WO-JP004732.
XX
PR 24-NOV-2000; 2000JP-00358539.
XX
(NISC-) JAPAN SCI & TECHNOLOGY CORP.
(NINA-) JAPAN NAT CENT NEUROLOGY & PSYCHIATRY.
PI Kaneko K;
XX
DR WPI; 2002-471742/50.
DR P-PSDB; AAC21548.
XX
PT Screening an antibody using 2-D electrophoresis on plural proteins in
PT samples for separating individual protein spots to react with an antibody
PT library useful in proteomics and other biological sciences.
XX
PS Disclosure; Fig 1; 78pp; Japanese.
XX
CC The invention relates to a novel method for screening an antibody,
CC comprising performing 2-D electrophoresis on plural proteins in a sample.
CC Individual protein spots are separated by reacting them with an antibody
CC library and then replicating the bound antibodies before reacting them
CC with the spot proteins again. The method is useful for screening an
CC antibody specific for a target protein, e.g. from a phage antibody
CC library, which is useful in proteomics for studying various proteins and
CC complementary deoxyribonucleic acid (cDNA) expression libraries as well
CC as gene functions, and in other biological and medical sciences. This

CC polynucleotide is a DNA sequence relating to the antibody screening
XX method of the invention
XX
SQ Sequence 348 BP; 71 A; 84 C; 108 G; 73 T; 0 U; 12 Other;
Query Match 69.8%; Score 247.2; DB 6; Length 348;
Best Local Similarity 82.6%; Pred. No. 5.4e-59;
Matches 289; Conservative 0; Mismatches 55; Indels 6; Gaps 1;
Qy 1 GAGGTGACGCTGGTGGAGTCTGGGGGGGCTTGGCAAGGCTGGGGGGTCCCTGAGACTC 60
Db 1 GAGGTGACGCTGGTGGAGTCTGGGGGGGCTTGGCAAGGCTGGGGGGTCCCTGAGACTC 60
Qy 61 TCCGTGCGAGCTCCGGGTTCCAGTTCACCTTCAATTAACCTACTACATGGACTGGTCCGC 120
Db 61 TCCGTGCGAGCTCTG-----GATTACCTTTAGAGCTATGCCATGAGCTGGTCCGC 114
Qy 121 CAGGCTCCAGGCGAGGCTGGAGTGGTCTCAGTATTAGTAGTATGGTATGCCACA 180
Db 115 CAGGCTCCAGGCGAGGCTGGAGTGGTCTCAGTATTAGTAGTATGGTATGCCACA 174
Qy 181 TGGTACGAGACTCCGTGAAGGCGAGATTCCACCATCTCCAGAGAGAACGCCAACACACA 240
Db 175 TACTACGAGACTCCGTGAAGGCGAGTTCCACCATCTCCAGAGAGAACGCCAACACAG 234
Qy 241 CTGTTTCTTCAATGAAACAGCTCAGAGCTGAGACACGGCTGTCTATTACTGTGCGAGC 300
Db 235 CTGTTTCTTCAATGAAACAGCTCAGAGCTGAGACACGGCTGTCTATTACTGTGCGAGC 294
Qy 301 TTGACTACAGGCTGAGCTCCGTGGGCGCAGGAGTCCGTGTCACCGCTC 350
Db 295 NNNNNNNNNNTTGGACTACTGGGGCGCAGGAAACCTGTGTCACCGCTC 344
RESULT 2
AAD46290
ID AAD46290 standard; DNA; 348 BP.
XX
AC AAD46290;
XX
XX 27-DEC-2002 (first entry)
XX Human KDR (VEGFR-2) Fab heavy chain (VH) DNA from D2C6 clone.
XX
XX Human; tumour; vascular endothelial growth factor receptor; metastasis;
XX epidermal growth factor receptor; non-small cell lung carcinoma; NSCLC;
XX breast; VEGFR; heart; EGFR; therapy; invasiveness; heavy chain; gene; VH;
XX ds.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..348
XX /*tag= a
XX /product= "Human KDR (VEGFR-2) Fab heavy chain (VH)
XX protein"
XX /note= "CDS does not include start and stop codon"
XX /partial
XX
XX WO200270008-A1.
XX
XX 12-SEP-2002.
XX
XX 04-MAR-2002; 2002WO-US006762.
XX
XX 02-MAR-2001; 2001US-00798689.
XX
XX (INCL-) INCLONE SYSTEMS INC.
XX (ROCK/) ROCKWELL P.
XX (GOLD/) GOLDSTEIN N I.
XX
XX WPI; 2002-691738/74.
XX P-PSDB; AAE28870.

XX Inhibiting tumor growth in humans involves administering vascular
PT endothelial growth factor receptor antagonists in combination with
PT radiation, chemotherapeutic agents, or epidermal growth factor receptor
PT antagonists.
XX Example 9; Page 121-122; 151pp; English.
XX The invention relates to a method of inhibiting tumour growth which
CC involves administering, vascular endothelial growth factor receptor
CC (VEGFR) antagonists in combination with radiation, chemotherapeutic
CC agent, or epidermal growth factor receptor (EGFR) antagonist. The method
CC is useful for inhibiting tumour growth in a human, where the tumour (e.g.
CC tumour of the breast, heart, lung, small intestine, colon, spleen, bone,
CC kidney, bladder, head and neck, ovary, prostate, brain, pancreas, skin,
CC bone marrow, blood, thymus, uterus, testicles, cervix or liver) over
CC expresses VEGFR. It is also useful for inhibiting growth of colon tumour
CC or non-small cell lung carcinoma (NSCLC) and tumour overexpressing EGFR.
CC It is preferably useful for treating subjects with both solid tumours,
CC preferably high vascular tumours and non-solid tumours. The inhibition or
CC reduction of tumour growth includes prevention or inhibition of the
CC progression of tumour, including cancerous and non-cancerous tumours,
CC where the progression of tumours includes the invasiveness, metastasis,
CC recurrence and increase in size of the tumour. The present sequence is
CC human KDR (VEGFR-2) Fab antibody heavy chain DNA
XX
SQ Sequence 348 BP; 82 A; 85 C; 105 G; 76 T; 0 U; 0 Other;
Query Match 68.2%; Score 241.6; DB 6; Length 348;
Best Local Similarity 82.9%; Pred. No. 2e-57;
Matches 290; Conservative 0; Mismatches 54; Indels 6; Gaps 1;
Qy 1 GAGGTGACGCTGGTGGAGTCTGGGGGGGCTTGGCAAGGCTGGGGGGTCCCTGAGACTC 60
Db 1 GAGGTGACGCTGGTGGAGTCTGGGGGGGCTTGGCAAGGCTGGGGGGTCCCTGAGACTC 60
Qy 61 TCCGTGCGAGCTCCGGGTTCCAGTTCACCTTCAATTAACCTACTACATGGACTGGTCCGC 120
Db 61 TCCGTGCGAGCTCTG-----GATTACCTTTAGAGCTATGCCATGAGCTGGTCCGC 114
Qy 121 CAGGCTCCAGGCGAGGCTGGAGTGGTCTCAGTATTAGTAGTATGGTATGCCACA 180
Db 115 CAGGCTCCAGGCGAGGCTGGAGTGGTCTCAGTATTAGTAGTATGGTATGCCACA 174
Qy 181 TGGTACGAGACTCCGTGAAGGCGAGATTCCACCATCTCCAGAGAGAACGCCAACACACA 240
Db 175 TACTACGAGACTCAGTGAAGGCGCGATTCCACCATCTCCAGAGAGAACGCCAACACTCA 234
Qy 241 CTGTTTCTTCAATGAAACAGCTCAGAGCTGAGACACGGCTGTCTATTACTGTGCGAGC 300
Db 235 CTGTTTCTTCAATGAAACAGCTCAGAGCTGAGACACGGCTGTCTATTACTGTGCGAGC 294
Qy 301 TTGACTACAGGCTGAGCTCCGTGGGCGCAGGAGTCCGTGTCACCGCTC 350
Db 295 GTCACAGATGCTTTTGGATATCTGGGGCGCAGGAGCAATGGTCCCGTCTC 344
RESULT 3
ABT23325
ID ABT23325 standard; DNA; 348 BP.
XX
AC ABT23325;
XX
XX 01-MAY-2003 (first entry)
XX
XX VEGF binding related DNA SEQ ID No 75.
XX
XX Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis;
XX leukaemia cell; vascular endothelial growth factor; tumour;
XX bispecific antigen-binding protein; human; gene; ds.
XX
XX Homo sapiens.
XX

PN W02003002144-A1.
 XX 09-JAN-2003.
 XX 26-JUN-2002; 2002WO-US020332.
 XX 26-JUN-2001; 2001US-0301299P.
 XX (IMCL-) IMCLONE SYSTEMS INC.
 XX Zhu Z;
 XX WPI; 2003-201468/19.
 DR P-PSDB; ABJ26763.
 XX New bispecific antibodies having antigen-binding sites specific for a
 PT first vascular endothelial growth factor (VEGF) receptor and for a second
 PT VEGF receptor, useful for inhibiting migration of leukemia cells, or for
 PT treating tumors.
 XX Disclosures; Page 70; 98pp; English.
 XX The invention relates to a novel antibody having a first antigen binding
 CC site specific for a first vascular endothelial growth factor (VEGF)
 CC receptor and a second antigen-binding site specific for a second VEGF
 CC receptor. The bispecific antigen-binding proteins block activation of the
 CC VEGF receptor and are useful for reducing or inhibiting VEGF-induced
 CC cellular functions such as mitogenesis of vascular endothelial cells and
 CC migration of leukaemia cells. The antibodies are useful for treating
 CC tumours and for in vivo or in vitro for investigative and diagnostic
 CC methods. This polynucleotide sequence represents a human DNA sequence
 CC relating to the bispecific antibodies that bind to the VEGF receptors of
 CC the invention
 XX
 XX Sequence 348 BP; 82 A; 85 C; 105 G; 76 T; 0 U; 0 Other;
 SQ
 Query Match 68.2%; Score 241.6; DB 7; Length 348;
 Best Local Similarity 82.9%; Pred. No. 2e-57;
 Matches 290; Conservative 0; Mismatches 54; Indels 6; Gaps 1;
 QY 1 GAGGTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTC 60
 DB 1 GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTGGTCAAGCCTGGGGGGTCCCTGAGACTC 60
 QY 61 TCCTGGCGAGCTCCGGGTTTCAGGTTTCACCTTCAATTAATCACTACTGAGTGGGTCCGC 120
 DB 61 TCCTGTGCAGCTCTG-----GATTTCCTTCAGTACATAGATGAATGGGTCCGC 114
 QY 121 CAGGCTCCAGGCGAGGGGCTGGAGTGGGTCTCAGTATTAGTAGTAGTGGTATCCCA 180
 DB 115 CAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCATCCATTAGTAGTAGTGGTATCCCA 174
 QY 181 TGGTACGAGACTCCGTGGAGGCGAGATTCCATCTCCAGAGAGAGCCCAACACACA 240
 DB 175 TACTACGAGACTCAGTGAAGGCGCATTCACCATCTCCAGAGAGAGCCCAACAGACTCA 234
 QY 241 CTGTTTCTTCAATGAACAGCTGAGAGTGGAGTGGAGTGGAGTGGTCTTATTACTGTGGAGC 300
 DB 235 CTGTATCTGCAATGACAGCTGAGCGAGGACACGCGTGTGTATTACTGTGGAGA 294
 QY 301 TTGACTACAGGGTCTGACTCTCTGGGGCGAGGAGTCTGTGTCACCGTCTC 350
 DB 295 GTCCACAGATGCTTTTGATATCTGGGGCCCAAGGGACAATGGTCAACCGTCTC 344
 RESULT 4
 ADD24416
 ID ADD24416 standard; DNA; 348 BP.
 XX
 XX ADD24416;
 XX
 XX 15-JAN-2004 (first entry)
 DT
 XX

DE Human heavy chain variable region DNA #2.
 XX
 KW tumour; vascular endothelial growth factor receptor; VEGFR;
 KW epidermal growth factor receptor; EGFR; cancer; human; ds; gene.
 XX
 OS Homo sapiens.
 XX
 PN US2003108545-A1.
 XX
 PD 12-JUN-2003.
 XX
 XX 04-MAR-2002; 2002US-00091300.
 PF
 XX 10-FEB-1994; 94US-00196041.
 PR 20-OCT-1994; 94US-00326552.
 PR 07-JUN-1995; 95US-00476533.
 PR 03-SEP-1996; 96US-00706804.
 PR 07-JAN-1997; 97US-00779450.
 PR 10-NOV-1997; 97US-00967113.
 PR 22-SEP-1999; 99US-00401163.
 PR 02-MAR-2001; 2001US-00798689.
 XX
 XX (ROCK/) ROCKWELL P.
 PA (GOLD/) GOLDSTEIN N I.
 PA
 XX Rockwell P, Goldstein NI;
 PI
 XX WPI; 2003-801265/75.
 DR P-PSDB; ADD24417.
 DR
 XX Inhibiting tumor growth by administering to a human a vascular
 PT endothelial growth factor receptor (VEGFR) antagonist and epidermal
 PT growth factor receptor (EGFR) antagonist.
 XX
 PS Example 12; SEQ ID NO 23; 90pp; English.
 XX
 CC The invention relates to a method of inhibiting tumour growth comprising
 CC administering to a human a vascular endothelial growth factor receptor
 CC (VEGFR) antagonist and epidermal growth factor receptor (EGFR)
 CC antagonist. The method is useful for inhibiting tumour growth. The
 CC present sequence is used in the exemplification of the invention.
 XX
 XX Sequence 348 BP; 82 A; 85 C; 105 G; 76 T; 0 U; 0 Other;
 SQ
 Query Match 68.2%; Score 241.6; DB 9; Length 348;
 Best Local Similarity 82.9%; Pred. No. 2e-57;
 Matches 290; Conservative 0; Mismatches 54; Indels 6; Gaps 1;
 QY 1 GAGGTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTC 60
 DB 1 GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTGGTCAAGCCTGGGGGGTCCCTGAGACTC 60
 QY 61 TCCTGGCGAGCTCCGGGTTTCAGGTTTCACCTTCAATTAATCACTACTGAGTGGGTCCGC 120
 DB 61 TCCTGTGCAGCTCTG-----GATTTCCTTCAGTACATAGATGAATGGGTCCGC 114
 QY 121 CAGGCTCCAGGCGAGGGGCTGGAGTGGGTCTCAGTATTAGTAGTAGTGGTATCCCA 180
 DB 115 CAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCATCCATTAGTAGTAGTGGTATCCCA 174
 QY 191 TGGTACGAGACTCCGTGGAGGCGAGATTCCATCTCCAGAGAGAGCCCAACACACA 240
 DB 175 TACTACGAGACTCAGTGAAGGCGCATTCACCATCTCCAGAGAGAGCCCAACAGACTCA 234
 QY 241 CTGTTTCTTCAATGAACAGCTGAGAGTGGAGTGGAGTGGAGTGGTCTTATTACTGTGGAGC 300
 DB 235 CTGTATCTGCAATGACAGCTGAGCGAGGACACGCGTGTGTATTACTGTGGAGA 294
 QY 301 TTGACTACAGGGTCTGACTCTCTGGGGCGAGGAGTCTGTGTCACCGTCTC 350
 DB 295 GTCCACAGATGCTTTTGATATCTGGGGCCCAAGGGACAATGGTCAACCGTCTC 344

RESULT 5
ADD80793
ID ADD80793 standard; DNA; 348 BP.
XX
AC ADD80793;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human clone D2C6 KDR-binding Fab variable heavy chain gene SEQ ID NO:23.
XX
KW human; antibody; KDR; cytostatic; gene therapy; anti-KDR antibody;
KW tumour; angiogenesis; gene; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..348
FT /tag= a
FT /product= "KDR-binding Fab"
FT /note= "No start/stop codon given"
XX
FN WO20003075840-A2.
PD 18-SEP-2003.
XX
PF 04-MAR-2003; 2003WO-US006459.
XX
PR 04-MAR-2002; 2002US-0361783P.
XX
PA (IMCL-) IMCLONE SYSTEMS INC.
XX
FI Zhu Z;
XX
WI WPI; 2003-779032/73.
DR P-PSDB; ADD80794.
XX
DE New human anti-KDR antibody, useful for preparing a composition for
PT reducing tumor growth and inhibiting angiogenesis.
XX
PS Claim 11; SEQ ID NO 23; 49pp; English.
XX
CC The invention relates to a novel isolated human antibody or its fragment
CC binds selectively to KDR. An antibody of the invention has cytostatic
CC activity, and may have a use in gene therapy. The antibody is anti-KDR
CC antibody. The antibody is useful for preparing a composition for reducing
CC tumor growth and inhibiting angiogenesis. The present sequence is used
CC in the exemplification of the invention.
XX
SQ Sequence 348 BP; 82 A; 85 C; 105 G; 76 T; 0 U; 0 Other;
Query Match 68.2%; Score 241.6; DB 9; Length 348;
Best Local Similarity 82.9%; Pred. No. 2e-57;
Matches 290; Conservative 0; Mismatches 54; Indels 6; Gaps 1;
QY 1 GAGGTGCGAGCTGGTGGAGTCTGGGGGGCTGGCAAGCCTGGGGGGTCCCTGAGACTC 60
DB |||||
1 GAGGTGCGAGCTGGTGGAGTCTGGGGGGCTGGCAAGCCTGGGGGGTCCCTGAGACTC 60
QY 61 TCCTGCGAGCTCCGGGTTGAGTTGACCTTCAATCACTACTGACTGAGTGGTCCGC 120
DB |||||
61 TCCTGCGAGCTCCG-----GATTCACCTTCAGTAGCTATAGCATGAGTGGTCCGC 114
QY 121 CAGGCTCCAGGCGAGGGCTGGAGTGGGTCTCACTATTAGTAGTGGTATCCACACA 180
DB |||||
115 CAGGCTCCAGGCGAGGGCTGGAGTGGGTCTCACTATTAGTAGTGGTATCCACACA 174
QY 181 TGGTAGCGAGACTCCGTGAAGGGCAGATTCCATCTCCAGAGAAAGCCCAACACA 240
DB |||||
175 TACTACGCGAGACTCAGTGAAGGGCGGATTCCATCTCCAGAGAAAGCCCAAGACTCA 234
QY 241 CTGTTTCTTCAATGAACAGCTGAGCTGAGGACCGGCTGCTATTACTGTGCGAGC 300
DB |||||
235 CTGTATCTGCAATGAACAGCTGAGGACCGGCTGCTATTACTGTGCGAGC 294

QY 301 TTGACTACAGGGTCTGACTCTCGGGCCAGGAGTCTGTCACCTCTC 350
DB |||||
295 GTACAGATGCTTTTGATATCTGGGCGCAAGGACAATGGTCACTCTC 344
RESULT 6
AAD46292
ID AAD46292 standard; DNA; 348 BP.
XX
AC AAD46292;
XX
DT 27-DEC-2002 (first entry)
XX
DE Human KDR (VEGFR-2) Fab heavy chain (VH) DNA from DIH4 clone.
XX
KW Human; tumour; vascular endothelial growth factor receptor; metastasis;
KW epidermal growth factor receptor; non-small cell lung carcinoma; NSCLC;
KW breast; VEGFR; heart; EGFR; therapy; invasiveness; heavy chain; gene; VH;
KW ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..348
FT /tag= a
FT /product= "Human KDR (VEGFR-2) Fab heavy chain (VH)
FT protein"
FT /note= "CDS does not include start and stop codon"
FT /partial
XX
FN WO200270008-A1.
PD 12-SEP-2002.
XX
PF 04-MAR-2002; 2002WO-US006762.
XX
PR 02-MAR-2001; 2001US-00798689.
XX
PA (IMCL-) IMCLONE SYSTEMS INC.
PA (ROCK/) ROCKWELL P.
PA (GOLD/) GOLDSTEIN N I.
XX
WI WPI; 2002-691738/74.
DR P-PSDB; AAE28870.
XX
DE Inhibiting tumor growth in humans involves administering vascular
PT endothelial growth factor receptor antagonists in combination with
PT radiation, chemotherapeutic agents, or epidermal growth factor receptor
PT antagonists.
XX
XX Example 12; Page 124-125; 151pp; English.
XX
CC The invention relates to a method of inhibiting tumour growth which
CC involves administering, vascular endothelial growth factor receptor
CC (VEGFR) antagonists in combination with radiation, chemotherapeutic
CC agent, or epidermal growth factor receptor (EGFR) antagonist. The method
CC is useful for inhibiting tumour growth in a human, where the tumour (e.g.
CC tumour of the breast, heart, lung, small intestine, colon, spleen, bone,
CC kidney, bladder, head and neck, ovary, prostate, brain, pancreas, skin,
CC bone marrow, blood, thymus, uterus, testicles, cervix or liver) over
CC expresses VEGFR. It is also useful for inhibiting growth of colon tumour
CC or non-small cell lung carcinoma (NSCLC) and tumour overexpressing EGFR.
CC It is preferably useful for treating subjects with both solid tumours,
CC preferably high vascular tumours and non-solid tumours. The inhibition or
CC reduction of tumour growth includes prevention or inhibition of the
CC progression of tumour, including cancerous and non-cancerous tumours,
CC where the progression of tumours includes the invasiveness, metastasis,
CC recurrence and increase in size of the tumour. The present sequence is
CC human KDR (VEGFR-2) Fab antibody heavy chain DNA
XX
SQ Sequence 348 BP; 82 A; 86 C; 104 G; 76 T; 0 U; 0 Other;

Query Match 67.8%; Score 240; DB 6; Length 348;
Best Local Similarity 82.6%; Pred. No. 5.5e-57;
Matches 289; Conservative 0; Mismatches 55; Indels 6; Gaps 1;
QY 1 GAGGTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAAGCCCTGGGGGGTCCCTGAGACTC 60
DB 1 GAGGTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAAGCCCTGGGGGGTCCCTGAGACTC 60
QY 61 TCCTGCGCAGCTCCGGGTTCCAGGTTCACTTCAATAAATAGTACTACATGGAGCTGGTCCGC 120
DB 61 TCCTGCGCAGCTCCGGGTTCCAGGTTCACTTCAATAAATAGTACTACATGGAGCTGGTCCGC 114
QY 121 CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTATCCACACA 180
DB 115 CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCATCCATTAGTAGTAGTGGTATCCACACA 174
QY 181 TGGTACGAGACTCCGTGAGGGCAGATTCAACCTCTCCAGAGGAGACGCCAACACACA 240
DB 175 TACTACGAGACTCAGTGAAGGCCCGATTCCATCTCCAGAGACAAACCCAGAACTCA 234
QY 241 CTGTTTCTTCAATGAACAGCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGC 300
DB 235 CTGTTTCTTCAATGAACAGCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGA 294
QY 301 TTGACTACAGGCTGCTGACTCTCGGGGCCAGGGAGTCTCGGTCAACCGTCTC 350
DB 295 GTACAGATGCTTTGATATCTGGGGCCAAAGGACAATGGTCAACCGTCTC 344

RESULT 7
ABT23327
ID ABT23327 standard; DNA; 348 BP.
XX AC ABT23327;
XX DT 01-MAY-2003 (first entry)
XX DE VEGF binding related DNA SEQ ID No 79.
XX KW Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis;
XX KW Leukemia cell; vascular endothelial growth factor; tumour;
XX KW bispecific antigen-binding protein; human; gene; ds.
XX OS Homo sapiens.
XX PN W02003002144-A1.
XX PD 09-JAN-2003.
XX PF 26-JUN-2002; 2002WO-US020332.
XX PR 26-JUN-2001; 2001US-0301299P.
XX PA (IMCL-) IMCLONE SYSTEMS INC.
XX PI Zhu Z;
XX DR WPI; 2003-201468/19.

New bispecific antibodies having antigen-binding sites specific for a first vascular endothelial growth factor (VEGF) receptor and for a second VEGF receptor, useful for inhibiting migration of leukemia cells, or for treating tumors.
PS Disclosure; Page 72; 98pp; English.
XX CC The invention relates to a novel antibody having a first antigen binding site specific for a first vascular endothelial growth factor (VEGF) receptor and a second antigen-binding site specific for a second VEGF receptor. The bispecific antigen-binding proteins block activation of the VEGF receptor and are useful for reducing or inhibiting VEGF-induced cellular functions such as mitogenesis of vascular endothelial cells and migration of leukaemia cells. The antibodies are useful for treating

tumours and for in vivo or in vitro for investigative and diagnostic methods. This polynucleotide sequence represents a human DNA sequence relating to the bispecific antibodies that bind to the VEGF receptors of the invention
XX SQ Sequence 348 BP; 82 A; 86 C; 104 G; 76 T; 0 U; 0 Other;
Query Match 67.8%; Score 240; DB 7; Length 348;
Best Local Similarity 82.6%; Pred. No. 5.5e-57;
Matches 289; Conservative 0; Mismatches 55; Indels 6; Gaps 1;
QY 1 GAGGTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAAGCCCTGGGGGGTCCCTGAGACTC 60
DB 1 GAGGTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAAGCCCTGGGGGGTCCCTGAGACTC 60
QY 61 TCCTGCGCAGCTCCGGGTTCCAGGTTCACTTCAATAAATAGTACTACATGGAGCTGGTCCGC 120
DB 61 TCCTGCGCAGCTCCGGGTTCCAGGTTCACTTCAATAAATAGTACTACATGGAGCTGGTCCGC 114
QY 121 CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTATCCACACA 180
DB 115 CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCATCCATTAGTAGTAGTGGTATCCACACA 174
QY 181 TGGTACGAGACTCCGTGAGGGCAGATTCAACCTCTCCAGAGGAGACGCCAACACACA 240
DB 175 TACTACGAGACTCAGTGAAGGCCCGATTCCATCTCCAGAGACAAACCCAGAACTCA 234
QY 241 CTGTTTCTTCAATGAACAGCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGC 300
DB 235 CTGTTTCTTCAATGAACAGCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGA 294
QY 301 TTGACTACAGGCTGCTGACTCTCGGGGCCAGGGAGTCTCGGTCAACCGTCTC 350
DB 295 GTACAGATGCTTTGATATCTGGGGCCAAAGGACAATGGTCAACCGTCTC 344

RESULT 8
ADD24420
ID ADD24420 standard; DNA; 348 BP.
XX AC ADD24420;
XX DT 15-JAN-2004 (first entry)
XX DE Human heavy chain variable region DNA #3.
XX KW tumour; vascular endothelial growth factor receptor; VEGFR;
XX KW epidermal growth factor receptor; EGFR; cancer; human; ds; gene.
XX OS Homo sapiens.
XX PN US2003108545-A1.
XX PD 12-JUN-2003.
XX PF 04-MAR-2002; 2002US-00091300.
XX PR 10-FEB-1994; 94US-00196041.
XX PR 20-OCT-1994; 94US-00326552.
XX PR 07-JUN-1995; 95US-00476533.
XX PR 03-SEP-1996; 96US-00706804.
XX PR 07-JAN-1997; 97US-00779450.
XX PR 10-NOV-1997; 97US-00967113.
XX PR 22-SEP-1999; 99US-00401163.
XX PR 02-MAR-2001; 2001US-00798689.
XX PA (ROCK/) ROCKWELL P.
XX PA (GOLD/) GOLDSTEIN N I.
XX PI Rockwell P, Goldstein NI;
XX DR WPI; 2003-801265/75.
XX DR P-PSDB; ADD24417.

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XX Inhibiting tumor growth by administering to a human a vascular
PT endothelial growth factor receptor (VEGFR) antagonist and epidermal
PT growth factor receptor (EGFR) antagonist.
XX Example 12; SEQ ID NO 27; 90pp; English.
XX The invention relates to a method of inhibiting tumour growth comprising
CC administering to a human a vascular endothelial growth factor receptor
CC (VEGFR) antagonist and epidermal growth factor receptor (EGFR)
CC antagonist. The method is useful for inhibiting tumour growth. The
CC present sequence is used in the exemplification of the invention.
XX
XX SQ Sequence 348 BP; 82 A; 86 C; 104 G; 76 T; 0 U; 0 Other;
      Query Match      67.8%; Score 240; DB 9; Length 348;
      Best Local Similarity 82.6%; Pred. No. 5.5e-57;
      Matches 289; Conservative 0; Mismatches 55; Indels 6; Gaps 1;

QY 1 GAGGTGACGCTGGTGGAGTCTGGGGGGGGCTGGCAAGCCTGGGGGGTCCCTGAGACTC 60
DB 1 GAGGTCCAGCTGGTGGAGTCTGGGGGGGGCTGGCAAGCCTGGGGGGTCCCTGAGACTC 60
QY 61 TCCTGCGCAGCTCCGGGTTTCAGGTTTCACCTTCAATAACTACTACATGACTGGGTCGGC 120
DB 61 TCCTGTGACGCTCTG-----GATTCACTTCAGTACTATAGCATGAACTGGTCCGCG 114
QY 121 CAGGCTCCAGGCGAGGGGTGGAGTGGTCTCAAGTATAGTATAGTGGTATCCACACA 180
DB 115 CAGGCTCCAGGCGAGGGGTGGAGTGGTCTCAAGTATAGTATAGTGGTATCCACACA 174
QY 181 TGGTACGACACTCCGTCGAAGGCGAGATTCACCATCTCCAGAGAGAACGCCCAACACACA 240
DB 175 TACTACGACACTCAGTGAAGGCGAGATTCACCATCTCCAGAGAGAACGCCCAACACTCA 234
QY 241 CTGTTTCTTCAATGAACAGCCTGAGAGCTGAGAGACACGGCTGTCTATTACTGTGGAGC 300
DB 235 CTGTATCTGCAATGAACAGCCTGAGAGCTGAGAGACACGGCTGTCTATTACTGTGGAGC 294
QY 301 TTGACTACAGGCTCTGACTCTCTGGGGCCAGGGAGTCTGTGTACCGTCTC 350
DB 295 GTACAGATGCTTTTGATATCTGGGGCCAGGGAGCAATGGTACCGTCTC 344

RESULT 9
ADD80797
ID ADD80797 standard; DNA; 348 BP.
XX AC ADD80797;
XX
XX 29-JAN-2004 (first entry)
XX
XX Human clone DIH4 KDR-binding Fab variable heavy chain gene SEQ ID NO:27.
XX
XX human; antibody; KDR; cytostatic; gene therapy; anti-KDR antibody;
XX tumour; angiogenesis; gene; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..348
XX /*tag= a
XX /product= "KDR-binding Fab"
XX /note= "No start/stop codon given"
XX
XX WO2003075840-A2.
XX
XX 18-SEP-2003.
XX
XX 04-MAR-2003; 2003WO-US006459.
XX
XX 04-MAR-2002; 2002US-0361783P.
XX

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PA (IMCL-) IMCLONE SYSTEMS INC.
XX
XX Zhu Z;
XX
XX WPI: 2003-779032/73.
XX P-PSDB; ADD80794.
XX
XX New human anti-KDR antibody, useful for preparing a composition for
XX reducing tumor growth and inhibiting angiogenesis.
XX
XX Example 1; SEQ ID NO 27; 49pp; English.
XX
XX The invention relates to a novel isolated human antibody or its fragment
XX binds selectively to KDR. An antibody of the invention has cytostatic
XX activity, and may have a use in gene therapy. The antibody is anti-KDR
XX antibody. The antibody is useful for preparing a composition for reducing
XX tumour growth and inhibiting angiogenesis. The present sequence is used
XX in the exemplification of the invention.
XX
XX SQ Sequence 348 BP; 82 A; 86 C; 104 G; 76 T; 0 U; 0 Other;
      Query Match      67.8%; Score 240; DB 9; Length 348;
      Best Local Similarity 82.6%; Pred. No. 5.5e-57;
      Matches 289; Conservative 0; Mismatches 55; Indels 6; Gaps 1;

QY 1 GAGGTGACGCTGGTGGAGTCTGGGGGGGGCTGGCAAGCCTGGGGGGTCCCTGAGACTC 60
DB 1 GAGGTCCAGCTGGTGGAGTCTGGGGGGGGCTGGCAAGCCTGGGGGGTCCCTGAGACTC 60
QY 61 TCCTGCGCAGCTCCGGGTTTCAGGTTTCACCTTCAATAACTACTACATGACTGGGTCGGC 120
DB 61 TCCTGTGACGCTCTG-----GATTCACTTCAGTACTATAGCATGAACTGGTCCGCG 114
QY 121 CAGGCTCCAGGCGAGGGGTGGAGTGGTCTCAAGTATAGTATAGTGGTATCCACACA 180
DB 115 CAGGCTCCAGGCGAGGGGTGGAGTGGTCTCAAGTATAGTATAGTGGTATCCACACA 174
QY 181 TGGTACGACACTCCGTCGAAGGCGAGATTCACCATCTCCAGAGAGAACGCCCAACACACA 240
DB 175 TACTACGACACTCAGTGAAGGCGAGATTCACCATCTCCAGAGAGAACGCCCAAGACTCA 234
QY 241 CTGTTTCTTCAATGAACAGCCTGAGAGCTGAGAGACACGGCTGTCTATTACTGTGGAGC 300
DB 235 CTGTATCTGCAATGAACAGCCTGAGAGCTGAGAGACACGGCTGTCTATTACTGTGGAGC 294
QY 301 TTGACTACAGGCTCTGACTCTCTGGGGCCAGGGAGTCTGTGTACCGTCTC 350
DB 295 GTACAGATGCTTTTGATATCTGGGGCCAGGGAGCAATGGTACCGTCTC 344

RESULT 10
ADD46294
ID ADD46294 standard; DNA; 348 BP.
XX AC ADD46294;
XX
XX 27-DEC-2002 (first entry)
XX
XX Human KDR (VEGFR-2) Fab heavy chain (VH) DNA from D2H2 clone.
XX
XX Human; tumour; vascular endothelial growth factor receptor; metastasis;
XX epidermal growth factor receptor; non-small cell lung carcinoma; NSCLC;
XX breast; VEGFR; heart; EGFR; therapy; invasiveness; heavy chain; gene; VH;
XX ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..348
XX /*tag= a
XX /product= "Human KDR (VEGFR-2) Fab heavy chain (VH)
XX protein"
XX /note= "CDS does not include start and stop codon"
XX

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FT XX /partial
PN XX WO200270008-A1.
XX XX 12-SEP-2002.
XX XX 04-MAR-2002; 2002WO-US0006762.
XX XX 02-MAR-2001; 2001US-00798689.
XX XX (IMCL-) IMCLONE SYSTEMS INC.
PA (ROCK/) ROCKWELL P.
PA (GOLD/) GOLDSTEIN N I.
XX XX WPI; 2002-691738/74.
DR P-PSDB; AAE28873.
XX XX Inhibiting tumor growth in humans involves administering vascular
PT endothelial growth factor receptor antagonists in combination with
PT radiation, chemotherapeutic agents, or epidermal growth factor receptor
PT antagonists.
XX XX Example 12; Page 126; 151pp; English.
XX XX The invention relates to a method of inhibiting tumour growth which
CC involves administering, vascular endothelial growth factor receptor
CC (VEGFR) antagonists in combination with radiation, chemotherapeutic
CC agent, or epidermal growth factor receptor (EGFR) antagonist. The method
CC is useful for inhibiting tumour growth in a human, where the tumour (e.g.
CC tumour of the breast, heart, lung, small intestine, colon, spleen, bone,
CC kidney, bladder, head and neck, ovary, prostate, brain, pancreas, skin,
CC bone marrow, blood, thymus, uterus, testicles, cervix or liver) over
CC expresses VEGFR. It is also useful for inhibiting growth of colon tumour
CC or non-small cell lung carcinoma (NSCLC) and tumour overexpressing EGFR.
CC It is preferably useful for treating subjects with both solid tumours,
CC reduction of tumour growth includes prevention or inhibition of the
CC progression of tumour, including cancerous and non-cancerous tumours,
CC where the progression of tumours includes the invasiveness, metastasis,
CC recurrence and increase in size of the tumour. The present sequence is
CC human XDR (VEGFR-2) Fab antibody heavy chain DNA
XX XX Sequence 348 BP; 82 A; 85 C; 105 G; 76 T; 0 U; 0 Other;
SQ
Query Match 67.3%; Score 238.4; DB 6; Length 348;
Best Local Similarity 82.3%; Pred. No. 1.5e-56;
Matches 288; Conservative 0; Mismatches 56; Indels 6; Gaps 1;
QY 1 GAGGTGAGCTGTGTGAGTCTGGGGCGGCTTGGCAAGCTTGGGGGGTCCCTGAGACTC 60
DB 1 GAAGTGACGCTGTGTGAGTCTGGGGGAGGCGCTGTGTCAAGCTTGGGGGGTCCCTGAGACTC 60
QY 61 TCCTGGCGAGCTCCCGGGTTCAGGTTTCACTTCAATAACTACTACATGAGCTGGGTCGCG 120
DB 61 TCCTGTGACGCTCTG-----GATTACCTTCAGTACTATAGCATGAGCTGGGTCGCG 114
QY 121 CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTACGTTATTAGTAGTGGTATCCCA 180
DB 115 CAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCATCCATTAGTAGTAGTATTACATA 174
QY 181 TGGTACGAGACTCCGTGAAGGCGAGATTCCACCATCTCCAGAGAACGCCAACACACA 240
DB 175 TACTAGCAGACTCAGTGAAGGGCCGATTCACCATCTCCAGAGAACGCCAGACTCA 234
QY 241 CTGTTTCTTCAAAATGAACGCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGC 300
DB 235 CTGTATCTGCAATGAACGCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGA 294
QY 301 TTGACTACAGGGTCTGACTCTCTGGGGCCAGGGAGTCTGTGTACCGTCTC 350
DB 295 GTACACATGCTTTTGATATCTCTGGGGCCAAAGGACAAATGGTACCGTCTC 344

RESULT 11
ABT23329
ID ABT23329 standard; DNA; 348 BP.
XX XX
AC ABT233329;
XX XX
DT 01-MAY-2003 (first entry)
XX XX
DE VEGF binding related DNA SEQ ID No 82.
XX XX
KW Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis;
KW leukaemia cell; vascular endothelial growth factor; tumour;
KW bispecific antigen-binding protein; human; gene; ds.
XX XX
OS Homo sapiens.
XX XX
PN WO2003002144-A1.
XX XX
PD 09-JAN-2003.
XX XX
PF 26-JUN-2002; 2002WO-US020332.
XX XX
PR 26-JUN-2001; 2001US-0301299P.
XX XX
PA (IMCL-) IMCLONE SYSTEMS INC.
XX XX
PI Zhu Z;
XX XX
DR WPI; 2003-201468/19.
DR P-PSDB; ABJ26765.
XX XX
PT New bispecific antibodies having antigen-binding sites specific for a
PT first vascular endothelial growth factor (VEGF) receptor and for a second
PT VEGF receptor, useful for inhibiting migration of leukemia cells, or for
PT treating tumors.
XX XX
PS Disclosure; Page 73-74; 98pp; English.
XX XX
CC The invention relates to a novel antibody having a first antigen binding
CC site specific for a first vascular endothelial growth factor (VEGF)
CC receptor and a second antigen-binding site specific for a second VEGF
CC receptor. The bispecific antigen-binding proteins block activation of the
CC VEGF receptor and are useful for reducing or inhibiting VEGF-induced
CC cellular functions such as mitogenesis of vascular endothelial cells and
CC migration of leukaemia cells. The antibodies are useful for treating
CC tumours and for in vivo or in vitro for investigative and diagnostic
CC methods. This polynucleotide sequence represents a human DNA sequence
CC relating to the bispecific antibodies that bind to the VEGF receptors of
CC the invention
XX XX
SQ Sequence 348 BP; 82 A; 85 C; 105 G; 76 T; 0 U; 0 Other;
Query Match 67.3%; Score 238.4; DB 7; Length 348;
Best Local Similarity 82.3%; Pred. No. 1.5e-56;
Matches 288; Conservative 0; Mismatches 56; Indels 6; Gaps 1;
QY 1 GAGGTGAGCTGTGTGAGTCTGGGGCGGCTTGGCAAGCTTGGGGGGTCCCTGAGACTC 60
DB 1 GAAGTGACGCTGTGTGAGTCTGGGGGAGGCGCTGTGTCAAGCTTGGGGGGTCCCTGAGACTC 60
QY 61 TCCTGGCGAGCTCCCGGGTTCAGGTTTCACTTCAATAACTACTACATGAGCTGGGTCGCG 120
DB 61 TCCTGTGACGCTCTG-----GATTACCTTCAGTACTATAGCATGAGCTGGGTCGCG 114
QY 121 CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTACGTTATTAGTAGTGGTATCCCA 180
DB 115 CAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCATCCATTAGTAGTAGTATTACATA 174
QY 181 TGGTACGAGACTCCGTGAAGGCGAGATTCCACCATCTCCAGAGAACGCCAACACACA 240
DB 175 TACTAGCAGACTCAGTGAAGGGCCGATTCACCATCTCCAGAGAACGCCAGACTCA 234
QY 241 CTGTTTCTTCAAAATGAACGCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGC 300

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Db 235 CTGTATCTGCAATGAACAGCCCTGAGAGCCGAGGACACGCTGTGTATTACTGTGGAGA 294
QY 301 TTGACTACAGGCTTGACTCTGGGGCCAGGGAGTCTGTGTACACCTCTC 350
Db 295 GTACACAGATGCTTTTGATATCTGGGGCCAAAGGACAAATGCTACCCGCTCTC 344

RESULT 12
ADD24423
ID ADD24423 standard; DNA; 348 BP.
AC ADD24423;
XX
XX
XX 15-JAN-2004 (first entry)
DE Human heavy chain variable region DNA #4.
KW tumour; vascular endothelial growth factor receptor; VEGFR;
KW epidermal growth factor receptor; EGFR; cancer; human; ds; gene.
XX
XX Homo sapiens.
XX
XX US2003108545-A1.
XX
XX 12-JUN-2003.
XX
XX 04-MAR-2002; 2002US-00091300.
XX
XX 10-FEB-1994; 94US-00196041.
XX 20-OCT-1994; 94US-00326552.
XX 07-JUN-1995; 95US-00476533.
XX 03-SEP-1996; 96US-00706804.
XX 07-JAN-1997; 97US-00779450.
XX 10-NOV-1997; 97US-00967113.
XX 22-SEP-1999; 99US-00401163.
XX 02-MAR-2001; 2001US-00798689.
XX
XX (ROCK/) ROCKWELL P.
XX (GOLD/) GOLDSTEIN N I.
XX
XX Rockwell P, Goldstein NI;
XX
XX WPI: 2003-801265/75.
XX P-PSDB; ADD24424.
XX
XX Inhibiting tumor growth by administering to a human a vascular
XX endothelial growth factor receptor (VEGFR) antagonist and epidermal
XX growth factor receptor (EGFR) antagonist.
XX
XX Example 12; SEQ ID NO 30; 90pp; English.
XX
XX The invention relates to a method of inhibiting tumour growth comprising
XX administering to a human a vascular endothelial growth factor receptor
XX (VEGFR) antagonist and epidermal growth factor receptor (EGFR)
XX antagonist. The method is useful for inhibiting tumour growth. The
XX present sequence is used in the exemplification of the invention.
XX
XX Sequence 348 BP; 82 A; 85 C; 105 G; 76 T; 0 U; 0 Other;
XX
XX Query Match 67.3%; Score 238.4; DB 9; Length 348;
XX Best Local Similarity 82.3%; Pred. No. 1.5e-56;
XX Matches 288; Conservative 0; Mismatches 56; Indels 6; Gaps 1;
XX
QY 1 GAGGTGCAGTGTGGAGTCTGGGGCGGCTTGGCAAGCCCTGGGGGGTCCCTGAGACTC 60
Db 1 GAAGTGCAGTGTGGAGTCTGGGGGAGGCGCTGTCAAGCTGGGGGGTCCCTGAGACTC 60
QY 61 TCCCTGGGCGACCTCCGGGTTCAAGTTCACCTTCAATCACTACTACATGACTGGTCCGC 120
Db 61 TCCCTGGGCGACCTCTG-----GATTCACCTTCAGTAGCTATAGCATGAATGGGTCCGC 114
QY 121 CAGGCTCCAGGGCAGCGGGCTGGAGTGGGTCTTCACCTATTAGTAGTAGTGGTATCCCA 180

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Db 115 CAGGCTCCAGGAGGGGCTGGAGTGGTCTCATCTAGTAGTAGTAGTACATTA 174
QY 181 TGGTACCCAGACTCCGCTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACACA 240
Db 175 TACTAOCAGACTCAGTGAAGGCCCGATTCCACCATCTCCAGAGACAACGCCAAGGACTCA 234
QY 241 CTGTTTCTTCAAAATGAACAGCCTGAGAGCTGAGGACACCGGCTGTCTATTACTGTGCGAGC 300
Db 235 CTGTATCTGCAATGAACAGCCTGAGAGCCGAGGACACCGCTGTGTATTACTGTGCGAGA 294
QY 301 TTGACTACAGGCTGTGACTCTCTGGGGCCAGGGAGTCTGTGTACACCTCTC 350
Db 295 GTACACAGATGCTTTTGATATCTGGGGCCAAAGGACAAATGCTACCCGCTCTC 344

RESULT 13
ADD80800
ID ADD80800 standard; DNA; 348 BP.
XX
XX AC ADD80800;
XX
XX 29-JAN-2004 (first entry)
DE Human clone D2H2 KDR-binding Fab variable heavy chain gene SEQ ID NO:30.
XX
XX human; antibody; KDR; cytostatic; gene therapy; anti-KDR antibody;
XX tumour; angiogenesis; gene; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..348
XX /*tag= a
XX /product= "KDR-binding Fab"
XX /note= "No start/stop codon given"
XX
XX WO2003075840-A2.
XX
XX 18-SEP-2003.
XX
XX 04-MAR-2003; 2003WO-US006459.
XX
XX 04-MAR-2002; 2002US-0361783P.
XX
XX (IMCL-) IMCLONE SYSTEMS INC.
XX
XX Zhu Z;
XX
XX WPI: 2003-779032/73.
XX P-PSDB; ADD80801.
XX
XX New human anti-KDR antibody, useful for preparing a composition for
XX reducing tumor growth and inhibiting angiogenesis.
XX
XX Example 1; SEQ ID NO 30; 49pp; English.
XX
XX The invention relates to a novel isolated human antibody or its fragment
XX binds selectively to KDR. An antibody of the invention has cytostatic
XX activity, and may have a use in gene therapy. The antibody is anti-KDR
XX antibody. The antibody is useful for preparing a composition for reducing
XX tumour growth and inhibiting angiogenesis. The present sequence is used
XX in the exemplification of the invention.
XX
XX Sequence 348 BP; 82 A; 85 C; 105 G; 76 T; 0 U; 0 Other;
XX
XX Query Match 67.3%; Score 238.4; DB 9; Length 348;
XX Best Local Similarity 82.3%; Pred. No. 1.5e-56;
XX Matches 288; Conservative 0; Mismatches 56; Indels 6; Gaps 1;
XX
QY 1 GAGGTGCAGTGTGGAGTCTGGGGCGGCTTGGCAAGCCCTGGGGGGTCCCTGAGACTC 60
Db 1 GAAGTGCAGTGTGGAGTCTGGGGGAGGCGCTGTGTCAAGCTGGGGGGTCCCTGAGACTC 60

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QY 61 TCCTGGCAGCCTCGGGTTTCAGGTTCACTTCAATAACTACTACATGAGCTGGGTCCGC 120
DB 61 TCCTGGCAGCCTCTG-----GATTCACCTTCAGTAGCTATAGCATGATGGGTCCGC 114
QY 121 CAGGCTCCAGGCGAGGGCTGGAGTGGGTCTCAGTATTAGTAGTGGTGGTATCCACCA 180
DB 115 CAGGCTCCAGGCGAGGGCTGGAGTGGGTCTCATCCATTAGTAGTAGTAGTATACATA 174
QY 181 TGGTACGGCAGACTCCGTTGAAGGCGCAGATTCCATCTCCAGAGAGAGCCCAACACACA 240
DB 175 TACTACGGCAGACTCAGTGAAGGCGCAGATTCCATCTCCAGAGAGAGCCCAACACACA 234
QY 241 CTGTTTCTTCAATGAACAGCCTGAGAGCTGAGGACACGCGTGTCTATTACTTGTGCGAGC 300
DB 235 CTGTTTCTTCAATGAACAGCCTGAGAGCTGAGGACACGCGTGTCTATTACTTGTGCGAGA 294
QY 301 TTGACTACAGGCTGTGACTCTCTGGGCGCAGGAGTCTCGTTCACCGTCTC 350
DB 295 GTACAGAGTCTTTTGATATCTCTGGGCGCAAGGAGCAATGGTCACCGTCTC 344

RESULT 14
AAS03478
ID AAS03478 standard; cDNA; 348 BP.
AC AAS03478;
XX AAS03478;
XX 29-AUG-2001 (first entry)
DE DNA encoding anti-adipocyte monoclonal antibody heavy chain, FAT 65.
XX Antibody; adipocyte; heavy chain; light chain; obesity; FAT;
KW heart disease; complementarity determining region; CDR; ss.
XX Homo sapiens.
XX WO200127279-A1.
XX 19-APR-2001.
XX 11-OCT-2000; 2000WO-08003900.
XX 12-OCT-1999; 99US-0158812P.
XX (CAME-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX Edwards BM, Main SH, Vaughan TJ;
PI WPI; 2001-282031/29.
DR P-PSDB; AAU02578.
XX Panel of specific binding members of antibody molecules which bind to
PT whole adipocytes is used in the treatment of obesity and obesity related
PT diseases.
XX Disclosure; Page 141; 182pp; English.

CC heart disease
XX Sequence 348 BP; 79 A; 91 C; 108 G; 70 T; 0 U; 0 Other;
SQ
Query Match 67.1%; Score 237.4; DB 4; Length 348;
Best Local Similarity 82.2%; Pred. No. 2.9e-56; Indels 6; Gaps 1;
Matches 287; Conservative 0; Mismatches 56;
QY 2 AGGTGCGAGCTGTGTGAGTCTGTGGGGCGGCTTGGCAAGCCCTGGGGGTCCCTGAGACTCT 61
DB 2 AGGTGCGAGCTGTGTGAGACCGGGGAGGCTTGGTCAAGCCTGGAGGGCCCTGAGACTTT 61
QY 62 CCTCGCAGCCTCCGGGTTTCAGGTTTCACCTTCAATAACTACTACATGAGCTGGGTCCGCC 121
DB 62 CCTGTGAGCCTCTG-----GATTCACCTTCAGTAGCTACTACATGAGCTGGGTCCGCC 115
QY 122 AGGCTCCAGGCGAGGGCTGGAGTGGGTCTCAGCTATTAGTAGTAGTGGTATCCACAT 181
DB 116 AGGCTCCAGGCGAGGGCTGGAGTGGGTCTCAGCTATTAGTAGTAGTGGTATCCACAA 175
QY 182 GGTACGCGAGCTCCGTGAAGGCGAGTTCACCATCTCCAGAGAGAGCCCAACACACAC 241
DB 176 ACTACGCGAGCTCTGTGAAGGCGCGATTTCACCATTTCCAGAGAGAGCCCAAGACTCAC 235
QY 242 TGTTCCTTCAATGAACAGCCTGAGAGCTGAGGACAGCGCTGTCTATTACTTGTGCGAGCT 301
DB 236 TGTATCTGCAATGAACAGCCTGAGAGCGCGAGGACAGCGCTGTCTATTACTTGTGCGAG 295
QY 302 TGACTACAGGCTGTGACTCTCTGGGCGCAGGAGTCTCTGTTCACCGTCTC 350
DB 296 ACGCGAGTGTGTCTGACCCCTGGGGCGCAGGCGACCCCTGGTTCACCGTCTC 344

RESULT 15
AAL43586
ID AAL43586 standard; DNA; 351 BP.
XX AAL43586;
XX AAL43586;
XX 05-SEP-2002 (first entry)
XX Dig3 antibody heavy chain coding sequence.
XX 26-10 scFv antibody light chain; complementarity determining region 3;
KW CDR3; binding protein production; catalytic protein production; ds;
KW Ligand structure determination; antibody isolation; dig3 heavy chain.
XX Unidentified.
XX Key Location/Qualifiers
FH 1.351
FT /tag= a
FT /partial
FT /product= "Dig3 heavy chain"
FT /note= "No start or stop codon is given"
XX WO200234886-A2.
XX 02-MAY-2002.
XX 26-OCT-2001; 2001WO-US046795.
XX 27-OCT-2000; 2000US-00699023.
XX (TEXA) UNIV TEXAS SYSTEM.
XX Chen G, Hayhurst A, Thomas JG, Iverson BL, Georgiou G;
XX WPI; 2002-500078/53.
XX P-PSDB; AAO15187.
XX Obtaining bacterium having nucleic acid encoding binding protein that
PT binds target ligand, or a nucleic acid encoding catalytic protein that

PT catalyzes reaction involving target substrate by display-less library
PT screening.
XX
XX Example 4; Page 97; 98pp; English.
XX
CC The invention comprises a method of obtaining a bacterium containing a
CC nucleic acid encoding a binding protein capable of binding a target
CC ligand, or a nucleic acid encoding a catalytic protein that catalyses a
CC reaction involving a target substrate. The method of the invention allows
CC the isolation of a cell expressing a nucleic acid encoding a binding
CC protein capable of binding a target ligand, and consequently the
CC isolation of the nucleic acid. The binding protein produced by the method
CC of the invention is useful in determining the structure of a target
CC ligand. The method of the invention is useful for the de novo isolation
CC of antibodies from large repertoire libraries and for monitoring
CC production during protein manufacturing. The method can also be used for
CC monitoring production of a particular byproduct of a biological reaction.
CC The present DNA sequence encodes the dig3 scFv antibody heavy chain which
CC is used in an example of the invention
XX
SQ Sequence 351 BP; 77 A; 85 C; 109 G; 80 T; 0 U; 0 Other;
Query Match 66.8%; Score 236.6; DB 6; Length 351;
Best Local Similarity 83.6%; Pred No. 4.9e-56;
Matches 295; Conservative 0; Mismatches 49; Indels 9; Gaps 2;
QY 1 GAGGTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCCTGGGGGGTCCCTGAGACTC 60
DB 1 GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCCTGGAGGCTCCCTGAGACTC 60
QY 61 TCCTGGCGAGCTCCGGGTTTCAGGTTCACTTCAATATCTACTATGAGTGGGTCCGC 120
DB 61 TCCTGGCGAGCTCTG-----GATTCACCTTCAGTGACTACTATGAGTGGGTCCGC 114
QY 121 CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTTATTAGTAGTGGTGTATCCACA 180
DB 115 CAGGCTCCAGGGAAGGGGCTGGAGTGGGTTTCATACATTAGTAGTGGTAGTACCATA 174
QY 181 TGGTAGCGAGACTCCGTGGAGGCGAGATTTCACCTCTCCAGAGAGAGCCCAACACACA 240
DB 175 TACTACGCGAGCTCTGTGAAGGCGGATTTCACCTCTCCAGGGAACGCCCAAGACTCA 234
QY 241 CTGTTTCTTCAATGAACAGCCTGAGAGCTGAGGACACCGCTGTCTATTACTGTGGAGC 300
DB 235 CTGTATCTGCAMATGAACAGCCTGAGAGCCGAGGACACCGCGGTGTATTACTGTGCAGA 294
QY 301 TTG---ACTACAGGGTCTGACTCTCTGGGCCAGGGAGTCTGGTCAACCGTCTC 350
DB 295 ACGGGTTTTCCGGGGTTTGACTATTGGGCCAAGGTACCTTGGTCAACCGTCTC 347

Search completed: June 19, 2004, 08:21:28
Job time : 283 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2004, 08:16:44 ; Search time 62 Seconds
(without alignments)
3168.591 Million cell updates/sec

Title: US-09-019-441A-7_COPY_58_411

Perfect score: 354

Sequence: 1 gaggtgacgtggaggagtc.....tccgtgacacgtctctca 354

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1059328

Minimum DB seq length: 0

Maximum DB seq length: 354

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:
5: /cgn2_6/ptodata/2/ina/PTUS_COMB.seq:
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	223.8	63.2	354	2	US-08-652-816A-21
2	223.2	63.1	354	2	US-08-652-816A-22
3	222.4	62.8	348	2	US-08-652-816A-24
4	215.4	60.8	351	2	US-08-428-197-35
5	215.4	60.8	351	5	PCT-US93-10555-35
6	214.2	60.5	345	2	US-08-428-197-41
7	214.2	60.5	345	5	PCT-US93-10555-41
8	213.6	60.3	294	2	US-08-428-197-47
9	213.6	60.3	294	5	PCT-US93-10555-47
10	212	59.9	354	2	US-08-958-201-1
11	200	56.5	354	2	US-08-958-201-3
12	196	55.4	348	2	US-09-184-658-10
13	196	55.4	348	4	US-09-504-262D-10
14	190	53.7	339	2	US-08-477-553A-52
15	187.8	53.1	351	3	US-09-240-274-184
16	186.8	52.8	285	3	US-09-043-514-1
17	186.8	52.8	306	2	US-08-273-146-64
18	185.4	52.4	354	4	US-09-530-139-21
19	183	51.7	351	4	US-09-339-922A-5
20	183	51.7	351	4	US-09-016-061-5
21	182.2	51.5	339	2	US-08-428-197-45
22	182.2	51.5	339	5	PCT-US93-10555-45
23	182.2	51.5	354	1	US-08-326-362-1
24	182.2	51.5	354	1	US-09-530-139-19
25	178.4	50.4	345	3	US-08-483-749A-5
26	178.4	50.4	351	4	US-09-339-922A-1
27					

28	178.4	50.4	351	4	US-08-791-391A-1
29	178.4	50.4	351	4	US-09-016-061-1
30	177.6	49.8	339	1	US-07-789-344A-9
31	176.2	49.3	335	2	US-08-477-553A-55
32	175.6	49.6	339	2	US-08-477-553A-54
33	171.4	48.4	342	2	US-08-477-553A-51
34	169.2	47.8	342	2	US-08-477-553A-53
35	168.2	47.5	354	5	PCT-US93-08435-9
36	167.8	47.4	342	4	US-09-530-139-17
37	165	46.6	297	3	US-09-042-353-139
38	165	46.6	297	4	US-08-758-417A-403
39	164.2	46.4	354	3	US-08-487-761-14
40	163.2	46.1	294	3	US-09-042-353-138
41	163.2	46.1	294	4	US-08-758-417A-402
42	162.4	45.9	318	1	US-08-129-930B-94
43	162.4	45.9	318	4	US-08-976-888A-94
44	161.4	45.6	294	3	US-09-042-353-132
45	161.4	45.6	294	3	US-09-042-353-136

ALIGNMENTS

RESULT 1
US-08-652-816A-21
; Sequence 21, Application US/08652816A
; Patent No. 5872215
; GENERAL INFORMATION:
; APPLICANT: Osbourn, JK
; APPLICANT: Allen, DJ
; TITLE OF INVENTION: Specific binding members, materials and
; TITLE OF INVENTION: methods.
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,816A
; FILING DATE: 23-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9125579.4
; FILING DATE: 02-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9125579.8
; FILING DATE: 02-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206372.6
; FILING DATE: 23-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9525004.9
; FILING DATE: 07-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9610824.6
; FILING DATE: 23-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/02240
; FILING DATE: 02-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/244,597
; FILING DATE: 01-JUN-1994
; ATTORNEY/AGENT INFORMATION:

Sequence 1, Appli
Sequence 1, Appli
Sequence 9, Appli
Sequence 55, Appli
Sequence 54, Appli
Sequence 51, Appli
Sequence 53, Appli
Sequence 9, Appli
Sequence 17, Appli
Sequence 139, App
Sequence 403, App
Sequence 14, Appli
Sequence 138, App
Sequence 402, App
Sequence 94, Appli
Sequence 94, Appli
Sequence 132, App
Sequence 136, App

Qy 187 GCAGCTCCGTAAGGCGCAGATTACCATCTCCAGAGAGAGCGCCAAACACACACTGTTT 246
 Db 181 GCGGACTCCGTAAGGCGCCGGTTCACTCACTCCAGAGAGAGCGCCAAACACACACTGTTT 240
 Qy 247 CTTCAATGTAAGGCGCAGATTACCATCTCCAGAGAGAGCGCCAAACACACACTGTTT 305
 Db 241 CTTCAATGTAAGGCGCAGATTACCATCTCCAGAGAGAGCGCCAAACACACACTGTTT 300
 Qy 306 --TACAGGGTCTGACTCTCCGCGGCGCAGAGAGTCTGCTCACCCTCTCTCTCA 354
 Db 301 TGGGATGCAATTTGATATCTGGGCGCCAGGAGCAATGTTTCACTCTCTCTCA 351

RESULT 5

PCT-US93-10555-35
 ; Sequence 35, Application PC/TUS9310555
 ; GENERAL INFORMATION:
 ; APPLICANT: SILVERMAN, GREGG J.
 ; TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
 ; TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
 ; TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERNATANT AND CONJUGATES
 ; TITLE OF INVENTION: THEREOF
 ; NUMBER OF SEQUENCES: 51
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Spensley Horn Jubb & Lubitz
 ; STREET: 1880 Century Park East - Suite 500
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 90067
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US93/10555
 ; FILING DATE: 29-OCT-1993
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Howells, Stacy L.
 ; REGISTRATION NUMBER: 34,842
 ; REFERENCE/DOCKET NUMBER: FD-2630
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 455-5100
 ; TELEFAX: (619) 455-5110
 ; INFORMATION FOR SEQ ID NO: 35:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 351 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; IMMEDIATE SOURCE:
 ; CLONE: SPA3-33
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 1..351
 ; PCT-US93-10555-35

Query Match 60.8%; Score 215.4; DB 5; Length 351;
 Best Local Similarity 80.1%; Pred. No. 8.2e-58;
 Matches 281; Conservative 0; Mismatches 61; Indels 9; Gaps 2;

Qy 7 CAGCTGGTGGAGTCTGGGGCGCGCTTGGCAAGCTGGGGGGTCCCTGAGACTCTCTGTC 66
 Db 7 CTGCTCGAGGAGTCTGGGGCGCGCTTGGTACAGCTGGGGTCCCTGAGACTCTCTGTC 66
 Qy 67 GCAGCTCCGCGGTTCAGGTTCACTTCAATACTACTACAGTGGTCCGCGAGCT 126
 Db 67 GAAGCTCTG-----GATTCCTTCAGTAATACTATGCGATGAGCTGGGTCGCGAGCT 120

Qy 127 CCAGGCGAGGGCTGGAGTGGTCTCACTATTAGTAGTAGTGGTATCCCAACATGGTAC 186
 Db 121 CCAGGCGAGGGCTGGAGTGGTCTCACTATTAGTAGTAGTGGTATCCCAACATGGTAC 180
 Qy 187 GCAGACTCCGTAAGGCGCAGATTACCATCTCCAGAGAGAGCGCCAAACACACTGTTT 246
 Db 181 GCGGACTCCGTAAGGCGCCGGTTCACTCACTCCAGAGAGAGCGCCAAACACTCTCTGTT 240
 Qy 247 CTTCAATGTAAGGCGCAGATTACCATCTCCAGAGAGAGCGCCAAACACTGTTT 305
 Db 241 CTTCAATGTAAGGCGCAGATTACCATCTCCAGAGAGAGCGCCAAACACTCTCTGTT 300
 Qy 306 --TACAGGGTCTGACTCTCCGCGGCGCAGGAGTCTGCTCACCCTCTCTCTCA 354
 Db 301 TGGGATGCAATTTGATATCTGGGCGCCAGGAGCAATGTTTCACTCTCTCTCA 351

RESULT 6

US-08-428-197-41
 ; Sequence 41, Application US/08428197
 ; Patent No. 5891438
 ; GENERAL INFORMATION:
 ; APPLICANT: SILVERMAN, GREGG J.
 ; TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
 ; TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
 ; TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERNATANT AND CONJUGATES
 ; TITLE OF INVENTION: THEREOF
 ; NUMBER OF SEQUENCES: 51
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Spensley Horn Jubb & Lubitz
 ; STREET: 1880 Century Park East - Suite 500
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 90067
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/428,197
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US93/10555
 ; FILING DATE: 29-OCT-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Howells, Stacy L.
 ; REGISTRATION NUMBER: 34,842
 ; REFERENCE/DOCKET NUMBER: FD-2630
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 455-5100
 ; TELEFAX: (619) 455-5110
 ; INFORMATION FOR SEQ ID NO: 41:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 345 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; IMMEDIATE SOURCE:
 ; CLONE: SP41-29
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 1..345
 ; US-08-428-197-41

Query Match 60.5%; Score 214.2; DB 2; Length 345;
 Best Local Similarity 79.6%; Pred. No. 1.9e-57;
 Matches 281; Conservative 0; Mismatches 63; Indels 9; Gaps 2;

Qy 2 AGGTGAGCTGGTGGAGTCTGGGGCGCGCTTGGCAAGCTGGGGGGTCCCTGAGACTCT 61


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Db      2 AGGTGAAGTCTGCTGAGTCTGGGGAGGCTTGGTACAGCTGGGGGTCCCTGAGACTCT 61
Qy      62 CTTGCGAGCTCCGGGTTCAAGTTCACTTCAATTAAGTCTTCAATGAGCTGGGTCCGCC 121
Db      62 CTTGCGAGCTCCG-----GATTCACTTTAGTAATTATGCCATGAGCTGGGTCCGCC 115
Qy      122 AGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCAGCTATTAGTAGTGGTATCCCAT 181
Db      116 AGGCTCCAGGGAGGGGCTGGAGTGGGTCTCAGCTATTAGTAGTGGTATCCCAT 175
Qy      182 GGTACGAGACTCCGTGAAGGCGAGATTCACTTCCAGAGAGAACGCCAACACAC 241
Db      176 ACTACGAGACTCCGTGAGGGCGCGTTCCGCTATCTCCAGAGACAAATTTCAAGAACACGC 235
Qy      242 TGTTCCTCAATGAAGACAGCTGAGCTGAGGACAGCTGCTTATTAATCTGTCGAGCT 301
Db      236 TGTATCTCAATGAAGACAGCTGAGGCGGAGGACAGCTGCTTATTAATCTGTCGAG 295
Qy      302 TGACTACAGGGTCTGACTCTCGGGCCAGGGAGTCCGTGTCACCGTCTCCTCA 354
Db      296 GATACAGCTACCTG---TCTGGGGCAAGGACCAAGCTCACCGTCTCCTCA 345

RESULT 7
PCT-US93-10555-41
; Sequence 41, Application PC/TUS9310555
; GENERAL INFORMATION:
; APPLICANT: SILVERMAN, GREGG J.
; TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
; TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
; TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East - Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10555
; FILING DATE: 29-OCT-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Howells, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: FD-2630
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 345 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: SpA1-29
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..345
PCT-US93-10555-41
Query Match 60.5%; Score 214.2; DB 5; Length 345;
Best Local Similarity 79.6%; Pred. No. 1.9e-57;

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Matches 281; Conservative 0; Mismatches 63; Indels 9; Gaps 2;
Qy      2 AGGTGAGCTGGTGGAGTCTGGGGGGGCTTGCAAGAGCTGGGGGTCCCTGAGACTCT 61
Db      2 AGGTGAAGTCTGCTGAGTCTGGGGAGGCTTGGTACAGCTGGGGGTCCCTGAGACTCT 61
Qy      62 CTTGCGAGCTCCGGGTTCAAGTTCACTTCAATTAAGTCTTCAATGAGCTGGGTCCGCC 121
Db      62 CTTGCGAGCTCCG-----GATTCACTTTAGTAATTATGCCATGAGCTGGGTCCGCC 115
Qy      122 AGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCAGCTATTAGTAGTGGTATCCCAT 181
Db      116 AGGCTCCAGGGAGGGGCTGGAGTGGGTCTCAGCTATTAGTAGTGGTATCCCAT 175
Qy      182 GGTACGAGACTCCGTGAAGGCGAGATTCACTTCCAGAGAGAACGCCAACACAC 241
Db      176 ACTACGAGACTCCGTGAGGGCGCGTTCCGCTATCTCCAGAGACAAATTTCAAGAACACGC 235
Qy      242 TGTTCCTCAATGAAGACAGCTGAGCTGAGGACAGCTGCTTATTAATCTGTCGAGCT 301
Db      236 TGTATCTCAATGAAGACAGCTGAGGCGGAGGACAGCTGCTTATTAATCTGTCGAG 295
Qy      302 TGACTACAGGGTCTGACTCTCGGGCCAGGGAGTCCGTGTCACCGTCTCCTCA 354
Db      296 GATACAGCTACCTG---TCTGGGGCAAGGACCAAGCTCACCGTCTCCTCA 345

RESULT 8
US-08-428-197-47
; Sequence 47, Application US/08428197
; Patent No. 5891438
; GENERAL INFORMATION:
; APPLICANT: SILVERMAN, GREGG J.
; TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
; TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
; TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East - Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/428,197
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10555
; FILING DATE: 29-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Howells, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: FD-2630
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 294 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: VH26C

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Best Local Similarity 78.6%; Pred. No. 9.5e-57;
Matches 283; Conservative 0; Mismatches 65; Indels 12; Gaps 2;
QY 1 GAGGTGCAGCTGGTGGAGTCTGGGGGGGGCTGGCAAGGCTGGGGGGTCCCTGAGACTC 60
Db 1 GAGGTGCAGCTGGTGGAGTCTGGGGGGGGCTGGTACAGCTGGGGGGTCCCTGAGACTC 60
QY 61 TCCTGGCAGCTCCGGGTTGAGTTCACTTCAATAACTACTACATGAGACTGGGTCGCG 120
Db 61 TCCTGGCAGCTCCGGGTTGAGTTCACTTCAATAACTACTACATGAGACTGGGTCGCG 114
QY 121 CAGGCTCCAGGGCAGGGGCTGGAGTGGTCTCACTATTAGTAGTGGTATCCACACA 180
Db 115 CAGGCTCCAGGGCAGGGGCTGGAGTGGTCTCACTATTAGTAGTGGTATCCACACA 174
QY 181 TGGTACGAGACTCCGGTGAAGGCGAGTTCACTATCTCCAGAGAGAACCCCAACACACA 240
Db 175 TACGAGCAGACTCCGGTGAAGGCGCGGTTCACTATCTCCAGGAGCAATTCAGAGACAG 234
QY 241 CTGTTCTTCAATGACAGCTGAGAGCTGAGAGTGGGCTGTCTATTACTGTGCGA-- 298
Db 235 GTGTACTGCAATGACAGCTGAGAGCTGAGAGTGGGCTGTCTATTACTGTGCGATT 294
QY 299 ----GCTTGACTACAGGTTGACTCTCTGGGGGCGAGGAGTCTGGTCACTGCTCTCA 354
Db 295 TTAGGAGTACTAAATGGTTTGTATATCTGGGGCGCAAGGGGCAATGGTCACTCTCTCA 354

RESULT 11
US-08-958-201-3
; Sequence 3, Application US/08958201
; Patent No. 5977319
; GENERAL INFORMATION:
; APPLICANT: Pope, Anthony R
; APPLICANT: Pritchard, Kevin
; APPLICANT: Williams, Andrew J
; APPLICANT: Johnson, Kevin S
; TITLE OF INVENTION: Specific binding members for estradiol;
; TITLE OF INVENTION: materials and methods
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-5402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/958,201
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,897
; FILING DATE: 21-OCT-1996
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 354 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: 1C
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..354
US-08-958-201-3

Query Match
Best Local Similarity 56.5%; Score 200; DB 2; Length 354;
Matches 283; Conservative 0; Mismatches 65; Indels 12; Gaps 2;

Matches 274; Conservative 0; Mismatches 74; Indels 12; Gaps 2;
QY 1 GAGGTGCAGCTGGTGGAGTCTGGGGGGGGCTGGCAAGGCTGGGGGGTCCCTGAGACTC 60
Db 1 GAGGTGCAGCTGGTGGAGTCTGGGGGGGGCTGGTACAGCTGGGGGGTCCCTGAGACTC 60
QY 61 TCCTGGCAGCTCCGGGTTGAGTTCACTTCAATAACTACTACATGAGACTGGGTCGCG 120
Db 61 TCCTGGCAGCTCCGGGTTGAGTTCACTTCAATAACTACTACATGAGACTGGGTCGCG 114
QY 121 CAGGCTCCAGGGCAGGGGCTGGAGTGGTCTCACTATTAGTAGTGGTATCCACACA 180
Db 115 CAGGCTCCAGGGCAGGGGCTGGAGTGGTCTCACTATTAGTAGTGGTATCCACACA 174
QY 181 TGGTACGAGACTCCGGTGAAGGCGAGTTCACTATCTCCAGAGAGAACCCCAACACACA 240
Db 175 NACCAAGCGGAGCTCCGGTGAAGGCGCGGTTCACTATCTCCAGGAGCAATTCAGAGACAG 234
QY 241 CTGTTCTTCAATGACAGCTGAGAGCTGAGAGTGGGCTGTCTATTACTGTGCGA-- 298
Db 235 GTGTACTGCAATGACAGCTGAGAGCTGAGAGTGGGCTGTCTATTACTGTGCGATT 294
QY 299 ----GCTTGACTACAGGTTGACTCTCTGGGGGCGAGGAGTCTGGTCACTGCTCTCA 354
Db 295 TTAGGAGTACTAAATGGTTTGTATATCTGGGGCGCAAGGGGCAATGGTCACTCTCTCA 354

RESULT 12
US-09-184-658-10
; Sequence 10, Application US/09184658
; Patent No. 6030792
; GENERAL INFORMATION:
; APPLICANT: Otterness, Ivan G.
; APPLICANT: Mezes, Peter S.
; APPLICANT: Downs, James T.
; APPLICANT: Johnson, Kimberly S.
; TITLE OF INVENTION: Assays for Measurement of Protein Fragments in
; FILE REFERENCE: PC9946-A
; CURRENT APPLICATION NUMBER: US/09/184,658
; CURRENT FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: 60/065,423
; EARLIER FILING DATE: 1997-11-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 348
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: V region
; LOCATION: (1)..(348)
; OTHER INFORMATION: Mature 5109 VH region.
US-09-184-658-10

Query Match
Best Local Similarity 55.4%; Score 196; DB 3; Length 348;
Matches 263; Conservative 0; Mismatches 85; Indels 6; Gaps 1;
QY 1 GAGGTGCAGCTGGTGGAGTCTGGGGGGGGCTGGCAAGGCTGGGGGGTCCCTGAGACTC 60
Db 1 GAGGTGCAGCTGGTGGAGTCTGGGGGGGGCTGGTACAGCTGGGGGGTCCCTGAGACTC 60
QY 61 TCCTGGCAGCTCCGGGTTGAGTTCACTTCAATAACTACTACATGAGACTGGGTCGCG 120
Db 61 TCCTGGCAGCTCCGGGTTGAGTTCACTTCAATAACTACTACATGAGACTGGGTCGCG 114
QY 121 CAGGCTCCAGGGCAGGGGCTGGAGTGGTCTCACTATTAGTAGTGGTATCCACACA 180
Db 115 CAGACTCCAGCAGAGAGCTGGAGTGGTCCGCAACCATTTATAGTATGGTGTCTCACC 174
QY 181 TGGTACGAGACTCCGGTGAAGGCGAGTTCACATCTCCAGAGAGAACCCCAACACACA 240

Mon Jun 21 11:45:43 2004

;; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

;; FILE REFERENCE: 09596-42U2

;; CURRENT APPLICATION NUMBER: US/09/240,274

;; EARLIER FILING DATE: 1999-01-29

;; EARLIER APPLICATION NUMBER: 60/081,380

;; EARLIER FILING DATE: 1998-04-10

;; EARLIER APPLICATION NUMBER: 60/028,550

;; EARLIER FILING DATE: 1996-10-11

;; NUMBER OF SEQ ID NOS: 224

;; SOFTWARE: PatentIn Ver. 2.0

;; SEQ ID NO 184

;; LENGTH: 351

;; TYPE: DNA

;; ORGANISM: Homo sapiens

;; FEATURE:

;; OTHER INFORMATION: anti-Rh(D) antibody clone SH17

;; FEATURE:

;; OTHER INFORMATION: anti-Rh(D) antibody clone SH17

;; US-09-240-274-184

Query Match 53.1%; Score 187.8; DB 3; Length 351;
Best Local Similarity 74.5%; Pred. No. 3.4e-49;
Matches 266; Conservative 0; Mismatches 82; Indels 9; Gaps 2;

QY	1	GAGGTGCAGCTGGTGGAGCTCGGGGCGGCTTGGCAAGCCTGGGGGGTCCCTGAGACTC	60
DB	1	GAGGTGCAGCTGGTGGAGCTCGGGGAGGCTTGGTCCAGCCCGGGGGTCCCTGAGACTC	60
QY	61	TCCTGGCGCAGCTCCGGGTTCAAGTTTCACTTCAATAACTACTATCATGGACTGGGTCCGC	120
DB	61	TCCTGGGTGCCTCTG-----GAATCCCTTTTCTTCTTGGATGGCTGGGTCCGC	114
QY	121	CAGGCTCCAGGGCAGGGGCTGGAGTGGTCTCAGCTATTAGTAGTAGTATCCACACA	180
DB	115	CAGGCCCCAGGGAAGGGGCTGGAGTGGTGGCCAAACATAAACAGATGGAAGTAAGAAA	174
QY	181	TGCTAGCGCAGACTCCGTGAAGGGCAGATTCAACATCTCCAGAGAGAAAGCCCAACACACA	240
DB	175	AACATATGTGACTCTCTGTGGAGGCCGATTCAACCTCTCCAGAGACAAACGGAAGACTCA	234
QY	241	CTGTTTCTTTCAATGAACAGCCTGAGCTGAGGACACGGCTGTCTATTACTGTGGAG-	299
DB	235	CTTTATCTGCAATGACAGCCTGAGAGCCGAGGACACGCGGATATATTACTGTGGCGGA	294
QY	300	--CTTGACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCTGTGTACCGTCTCCTCA	354
DB	295	GATTCACTTACTTGTGTTTGTACTCTGGGCCAGGAGCCCTGGTCAACCGTCTCCTCA	351

Search completed: June 19, 2004, 09:58:55
Job time : 64 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2004, 08:52:24 ; Search time 285 Seconds
(without alignments)
5890.195 Million cell updates/sec

Title: US-09-019-441a-7_COPY_58_411

Perfect score: 354

Sequence: 1 gaggtgcagctggggagtc.....tctgtgacacgtctctca 354

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 2593982

Minimum DB seq length: 0

Maximum DB seq length: 354

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*

- 1: /cgn2_6/prodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/prodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/prodata/2/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/prodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/prodata/2/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/prodata/2/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/prodata/2/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/prodata/2/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/prodata/2/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/prodata/2/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/prodata/2/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/prodata/2/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/prodata/2/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/prodata/2/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/prodata/2/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/prodata/2/pubpna/US10_NEW_PUB.seq.*
- 17: /cgn2_6/prodata/2/pubpna/US10_PUBCOMB.seq.*
- 18: /cgn2_6/prodata/2/pubpna/US60_NEW_PUB.seq.*
- 19: /cgn2_6/prodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	241.6	68.2	348	15	US-10-091-300-23
2	240	67.8	348	15	Sequence 23, Appl
3	238.4	67.3	348	15	Sequence 27, Appl
4	232.6	65.7	351	17	US-10-091-300-30
5	223.8	63.2	349	12	US-10-466-836-25
6	223.8	63.2	349	12	Sequence 25, Appl
7	222.6	62.9	294	16	US-10-269-711-18
8	222.6	62.9	311	9	Sequence 18, Appl
9	221.6	62.6	296	17	US-10-251-215-17
10	219.4	62.0	294	15	Sequence 17, Appl
11	219	61.9	348	15	Sequence 3233, A
12	218.4	61.7	345	15	Sequence 29, Appl
13	218.2	61.6	351	15	Sequence 20, Appl
14	216.8	61.2	296	13	Sequence 15, Appl
					Sequence 11, Appl
					Sequence 23, Appl
					Sequence 1, Appl

15	216.8	61.2	296	17	US-10-038-591-31	Sequence 31, Appl
16	215.8	61.0	354	15	US-10-120-377-74	Sequence 74, Appl
17	214.4	60.6	345	17	US-10-408-901-17	Sequence 17, Appl
18	211.4	59.7	291	16	US-10-251-215-18	Sequence 18, Appl
19	211.4	59.7	327	15	US-10-029-386-24519	Sequence 24519, A
20	208.4	59.2	348	17	US-10-408-901-13	Sequence 13, Appl
21	208.8	59.0	302	17	US-10-432-409A-175	Sequence 175, Appl
22	207.8	58.7	354	15	US-10-324-493-7	Sequence 7, Appl
23	205.6	58.1	348	16	US-10-338-366-1	Sequence 1, Appl
24	205	57.9	291	16	US-10-251-215-21	Sequence 21, Appl
25	204	57.6	302	17	US-10-432-409A-170	Sequence 170, Appl
26	203.6	57.5	345	9	US-09-974-449-1	Sequence 1, Appl
27	202.8	57.3	342	13	US-10-147-849-4	Sequence 4, Appl
28	200.8	56.7	354	16	US-10-173-551-13	Sequence 13, Appl
29	200	56.5	345	17	US-10-408-901-9	Sequence 9, Appl
30	198.2	56.0	348	17	US-10-408-901-21	Sequence 21, Appl
31	197.6	55.8	294	13	US-09-948-939-14	Sequence 14, Appl
32	197.6	55.8	296	13	US-09-948-939-20	Sequence 20, Appl
33	197.6	55.8	296	15	US-10-320-094-12	Sequence 12, Appl
34	197.6	55.8	329	15	US-10-010-729-34	Sequence 34, Appl
35	195.4	55.2	294	10	US-09-995-529-7	Sequence 7, Appl
36	195.4	55.2	294	13	US-09-948-939-2	Sequence 2, Appl
37	195.2	55.1	349	12	US-10-408-901-5	Sequence 5, Appl
38	195	55.1	348	17	US-10-338-366-51	Sequence 51, Appl
39	193.8	54.7	294	16	US-10-408-901-25	Sequence 25, Appl
40	193.4	54.6	348	17	US-10-408-901-25	Sequence 25539, A
41	192.2	54.3	305	9	US-09-864-761-22022	Sequence 22022, A
42	192.2	54.3	308	15	US-10-029-386-25539	Sequence 25539, A
43	191	54.0	288	16	US-10-251-215-19	Sequence 19, Appl
44	189.2	53.4	351	13	US-10-257-864A-55	Sequence 55, Appl
45	189.2	53.4	351	17	US-10-399-518-55	Sequence 55, Appl

ALIGNMENTS

RESULT 1

US-10-091-300-23
; Sequence 23, Application US/10091300
; Publication No. US20030108545A1
; GENERAL INFORMATION:
; APPLICANT: Rockwell, Patricia
; TITLE OF INVENTION: Combination Methods of Inhibiting Tumor Growth With a Vascular
; FILE OF INVENTION: Endothelial Growth Factor Receptor Antagonist
; FILE REFERENCE: 11245/46211
; CURRENT APPLICATION NUMBER: US/10/091,300
; CURRENT FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 23
; TYPE: DNA
; ORGANISM: Human
US-10-091-300-23

Query Match 68.2%; Score 241.6; DB 15; Length 348;
Best Local Similarity 82.9%; Pred. No. 1.8e-66;
Matches 290; Conservative 0; Mismatches 54; Indels 6; Gaps 1;

QY	1	GAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAGCCCTGGGGGGTCCCTGAGACTC	60
DB	1		60
QY	61	TCCTGCGCAGCTCCGGGTTACAGTTTCACCTTCAATAACTACTATACATGACTGGGTCCGC	120
DB	61		114
QY	121	CAGGCTCCAGGCGAGGCGCTGGAGTGGGTCTCCACCTATTAGTAGTGTGTATCCACA	180
DB	115		174
QY	181	TGTAAGCAGACTCCGTGAAGGCGAGTTCACCATCTCCAGAGAGAACCCCAACACA	240

Db 175 TACTACGAGACTCAGTGAAGGCGGATTCACCATCTCCAGAGACAACGCCAAGACTCA 234
Qy 241 CTGTTCTTCAATGACAGCCTGAGAGCTGAGGACACGGCTCTCTATTACTGTGGAGC 300
Db 235 CTGTATCTGCAATGACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGGAGA 294
Qy 301 TTGACTACAGGCTCTGACTCTCGGGGCGAGGAGTCTCTGGTCAACCGTCTC 350
Db 295 GTACAGATGCTTTTGATATCTGGGCGCAAGGACATGCTACCGTCTC 344

RESULT 2
US-10-091-300-27
; Sequence 27, Application US/10091300
; Publication No. US20030108545A1
; GENERAL INFORMATION:
; APPLICANT: Rockwell, Patricia
; APPLICANT: Goldstein, Neil I.
; TITLE OF INVENTION: Combination Methods of Inhibiting Tumor Growth With a Vascular
; TITLE OF INVENTION: Endothelial Growth Factor Receptor Antagonist
; FILE REFERENCE: 11245/46211
; CURRENT APPLICATION NUMBER: US/10/091,300
; CURRENT FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 27
; LENGTH: 348
; TYPE: DNA
; ORGANISM: Human
US-10-091-300-27

Query Match 67.8%; Score 240; DB 15; Length 348;
Best Local Similarity 82.6%; Pred. No. 5.8e-66;
Matches 289; Conservative 0; Mismatches 55; Indels 6; Gaps 1;
Qy 1 GAGGTGAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCTCGGGGGTCCCTGAGACTC 60
Db 1 GAGGTGAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCTCGGGGGTCCCTGAGACTC 60
Qy 61 TCCTGCGCAGCTCCGGGTTTCAGGTTTCACTTCAATAACTACTATACATGAGACTGGGTCCGC 120
Db 61 TCCTGCGCAGCTCTG-----GATTCACCTTCAGTAGCTATAGCATGAGTGGTCCGC 114
Qy 121 CAGGCTCCAGGCGAGGCTGGAGTGGTCTACGATTTAGTAGTAGTGGTATCCACA 180
Db 115 CAGGCTCCAGGCGAGGCTGGAGTGGTCTATCCATTAGTAGTAGTATTACATA 174
Qy 181 TGGTACGACACTCCGTGAAGGCGAGATTCACCATCTCCAGAGAGAACGCCAACACACA 240
Db 175 TACTACGACACTCAGTGAAGGCGGATTCACCATCTCCAGAGACAACGCCAAGACTCA 234
Qy 241 CTGTTCTTCAATGACAGCCTGAGAGCTGAGGACACGGCTCTCTATTACTGTGGAGC 300
Db 235 CTGTATCTGCAATGACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGGAGA 294
Qy 301 TTGACTACAGGCTCTGACTCTCGGGCGAGGAGTCTCTGGTCAACCGTCTC 350
Db 295 GTACAGATGCTTTTGATATCTGGGCGCAAGGACATGCTACCGTCTC 344

RESULT 3
US-10-091-300-30
; Sequence 30, Application US/10091300
; Publication No. US20030108545A1
; GENERAL INFORMATION:
; APPLICANT: Rockwell, Patricia
; APPLICANT: Goldstein, Neil I.
; TITLE OF INVENTION: Combination Methods of Inhibiting Tumor Growth With a Vascular
; TITLE OF INVENTION: Endothelial Growth Factor Receptor Antagonist
; FILE REFERENCE: 11245/46211
; CURRENT APPLICATION NUMBER: US/10/091,300
; CURRENT FILING DATE: 2002-03-04

; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 30
; LENGTH: 348
; TYPE: DNA
; ORGANISM: Human
US-10-091-300-30

Query Match 67.3%; Score 238.4; DB 15; Length 348;
Best Local Similarity 82.3%; Pred. No. 1.9e-65;
Matches 288; Conservative 0; Mismatches 56; Indels 6; Gaps 1;
Qy 1 GAGGTGAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCTCGGGGGTCCCTGAGACTC 60
Db 1 GAGGTGAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCTCGGGGGTCCCTGAGACTC 60
Qy 61 TCCTGCGCAGCTCCGGGTTTCAGGTTTCACTTCAATAACTACTATACATGAGACTGGGTCCGC 120
Db 61 TCCTGCGCAGCTCTG-----GATTCACCTTCAGTAGCTATAGCATGAGTGGTCCGC 114
Qy 121 CAGGCTCCAGGCGAGGCTGGAGTGGTCTACGATTTAGTAGTAGTGGTATCCACA 180
Db 115 CAGGCTCCAGGCGAGGCTGGAGTGGTCTATCCATTAGTAGTAGTATTACATA 174
Qy 181 TGGTACGACACTCCGTGAAGGCGAGATTCACCATCTCCAGAGAGAACGCCAACACACA 240
Db 175 TACTACGACACTCAGTGAAGGCGGATTCACCATCTCCAGAGACAACGCCAAGACTCA 234
Qy 241 CTGTTCTTCAATGACAGCCTGAGAGCTGAGGACACGGCTCTCTATTACTGTGGAGC 300
Db 235 CTGTATCTGCAATGACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGGAGA 294
Qy 301 TTGACTACAGGCTCTGACTCTCGGGCGAGGAGTCTCTGGTCAACCGTCTC 350
Db 295 GTACAGATGCTTTTGATATCTGGGCGCAAGGACATGCTACCGTCTC 344

RESULT 4
US-10-466-836-25
; Sequence 25, Application US/10466836
; Publication No. US20040110922A1
; GENERAL INFORMATION:
; APPLICANT: GAVISH-GALILEE BIO-APPLICATIONS LTD.
; TITLE OF INVENTION: CHIMERIC PROTEINS FOR PREVENTION AND TREATMENT OF HIV INFECTION
; FILE REFERENCE: GAVISH-003 PCT
; CURRENT APPLICATION NUMBER: US/10/466,836
; CURRENT FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Version 3.1
; SEQ ID NO 25
; LENGTH: 351
; TYPE: DNA
; ORGANISM: HUMAN
US-10-466-836-25

Query Match 65.7%; Score 232.6; DB 17; Length 351;
Best Local Similarity 82.4%; Pred. No. 1.3e-63;
Matches 294; Conservative 0; Mismatches 54; Indels 9; Gaps 2;
Qy 1 GAGGTGAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCTCGGGGGTCCCTGAGACTC 60
Db 1 GAGGTGAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTC 60
Qy 61 TCCTGCGCAGCTCCGGGTTTCAGGTTTCACTTCAATAACTACTATACATGAGACTGGGTCCGC 120
Db 61 TCCTGCGCAGCTCTG-----GATTCACCTTTAGCAGCTATGCCATGAGTGGGTCCGC 114
Qy 121 CAGGCTCCAGGCGAGGCTGGAGTGGTCTCACGATTTAGTAGTAGTGGTATCCACA 180
Db 115 CAGGCTCCAGGCGAGGCTGGAGTGGTCTCAGCTATTAGTGGTGGTGGTAGCACA 174

QY 181 TGGTACGAGACTCGTGAAGGCGGAGTTCACCATCTCCAGAGAGAGCGCAACACACA 240
DB 175 TACTACGAGACTCGTGAAGGCGGAGTTCACCATCTCCAGAGAGAGCGCAACACAG 234
QY 241 CTGTTTCTTCAATGAACAGAGCTGAGAGCTGAGAGACAGCGGTGCTATTACTGTGCA-- 298
DB 235 CTGTATCTGCAATGAACAGAGCTGAGAGCGGAGAGACAGCGCGGTGCTATTACTGTGCA 294
QY 299 -GCTTGACTACAGGCTGAGTCTCTGGGGGCGAGAGTCTGCTGACCGTCTCTCA 354
DB 295 CGGGGCGATCGTGTCTTTGACTATTGGGGGCGAGGTACCGTCTGCTCTCTCA 351

RESULT 5

US-10-269-711-18
; Sequence 18, Application US/10269711
; Publication No. US20040071694A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Devries, Peter J.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Ostrow, Dave
; APPLICANT: Weiler, James
; APPLICANT: Green, Larry
; TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR BINDING
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 6989.US.O1
; CURRENT APPLICATION NUMBER: US/10/269,711
; CURRENT FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 349
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-269-711-18

Query Match 63.2%; Score 223.8; DB 12; Length 349;
Best Local Similarity 79.3%; Pred. No. 8.1e-61;
Matches 280; Conservative 0; Mismatches 67; Indels 6; Gaps 1;

QY 2 AGGTGCAAGTCTGGAGTCTGGGGGCGGCTTGGCAAGCGCTGGGGGCTCCCTGAGACTCT 61
DB 2 AGGTGCAAGTCTGGAGTCTGGGGGCGGCTTGGCAAGCGCTGGGGGCTCCCTGAGACTCT 61
QY 62 CCTGCGAGCTCCGCTGAGGCTGAGTTCACCTTCAATTAATGCTGAGTCTCCGCGC 121
DB 62 CCTGCGAGCTCCGCTGAGGCTGAGTTCACCTTCAATTAATGCTGAGTCTCCGCGC 115
QY 122 AGGTCCAGGCGAGGCGCTGGAGTGGTCTCACTATTAGTGTGATGATGATGATGAT 181
DB 116 AGGTCCAGGCGAGGCGCTGGAGTGGTCTCACTATTAGTGTGATGATGATGATGAT 175
QY 182 GGTACGAGACTCCGCTGAGAGGAGATTACACCTCCAGAGAGAGCGCAACACACAC 241
DB 176 ACTATGAGACTCCGCTGAGAGGCGGATTCACCTTCCAGAGAGATTCCAGAGAGCGC 235
QY 242 TGTTTCTTCAATGAACAGAGCTGAGAGCTGAGAGAGCGGTGCTATTACTGTGCGAGT 301
DB 236 TGTATCTGCAATGAACAGAGCTGAGAGCGGAGAGAGCGGTGCTATTACTGTGCGAG 295
QY 302 TGACTACAGGCTCTGACTCTGGGGGCGAGGAGTCTGCTGCTCCTCTCA 354
DB 296 GTCCGTACTACTTGTACTTGTGGGCGGAGGAGCGGCTGCTCCTCTCTCA 348

RESULT 6

US-10-269-711-38
; Sequence 38, Application US/10269711
; Publication No. US20040071694A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Devries, Peter J.

; APPLICANT: Reilly, Edward B.
; APPLICANT: Ostrow, Dave
; APPLICANT: Weiler, James
; APPLICANT: Green, Larry
; TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR BINDING
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 6989.US.O1
; CURRENT APPLICATION NUMBER: US/10/269,711
; CURRENT FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 349
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-269-711-38

Query Match 63.2%; Score 223.8; DB 12; Length 349;
Best Local Similarity 79.3%; Pred. No. 8.1e-61;
Matches 280; Conservative 0; Mismatches 67; Indels 6; Gaps 1;

QY 2 AGGTGCAAGTCTGGAGTCTGGGGGCGGCTTGGCAAGCGCTGGGGGCTCCCTGAGACTCT 61
DB 2 AGGTGCAAGTCTGGAGTCTGGGGGCGGCTTGGCAAGCGCTGGGGGCTCCCTGAGACTCT 61
QY 62 CCTGCGAGCTCCGCTGAGGCTGAGTTCACCTTCAATTAATGCTGAGTCTCCGCGC 121
DB 62 CCTGCGAGCTCCGCTGAGGCTGAGTTCACCTTCAATTAATGCTGAGTCTCCGCGC 115
QY 122 AGGTCCAGGCGAGGCGCTGGAGTGGTCTCACTATTAGTGTGATGATGATGATGAT 181
DB 116 AGGTCCAGGCGAGGCGCTGGAGTGGTCTCACTATTAGTGTGATGATGATGATGAT 175
QY 182 GGTACGAGACTCCGCTGAGAGGAGATTACACCTCCAGAGAGAGCGCAACACACAC 241
DB 176 TGTATCTGCAATGAACAGAGCTGAGAGCGGATTCACCTTCCAGAGAGATTCCAGAG 235
QY 242 TGTTTCTTCAATGAACAGAGCTGAGAGCTGAGAGAGCGGTGCTATTACTGTGCGAGT 301
DB 236 TGTATCTGCAATGAACAGAGCTGAGAGCGGATTCACCTTCCAGAGAGATTCCAGAG 295
QY 302 TGACTACAGGCTCTGACTCTGGGGGCGAGGAGTCTGCTGCTCCTCTCA 354
DB 296 GCGGGAGCTACTGGGAGCTACTGGGGGCGAGGAGCGGCTGCTCCTCTCA 348

RESULT 7

US-10-251-215-17
; Sequence 17, Application US/10251215
; Publication No. US20030219839A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Kretz-Rommel, Anke
; APPLICANT: Frederickson, Shana
; TITLE OF INVENTION: ANTI-PDGF ANTIBODIES AND METHODS FOR PRODUCING ENGINEERED
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 1087-36
; CURRENT APPLICATION NUMBER: US/10/251,215
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 60/323,537
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: US 60/323,544
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: US 60/379,980
; PRIOR FILING DATE: 2002-05-13
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 294
; TYPE: DNA
; ORGANISM: human
US-10-251-215-17

Query Match 62.9%; Score 222.6; DB 16; Length 294;
 Best Local Similarity 86.6%; Pred. No. 1.9e-60;
 Matches 259; Conservative 0; Mismatches 34; Indels 6; Gaps 1;
 QY 1 GAGGTCCAGCTGTGGAGCTCTGGGGCGCTTGGCAAGCCCTGGGGGTCCTCAGACTC 60
 Db 1 GAGGTCCAGCTGTGGAGCTCTGGGGCGCTTGGCAAGCCCTGGGGGTCCTCAGACTC 60
 QY 61 TCTGCGCAGCTCTCCGGGTTCAAGTTCACTTCAATTAATCTATCATGACTGGGTCCGC 120
 Db 61 TCTGTCGAGCTCTG-----GATTCACCTTCAGTAGTATAGATGAATGGTCCGC 114
 QY 121 CAGGCTCCAGGCGAGGGCTGGAGTGGTCTCAGCTATAGTAGTGGTGGTATCCACACA 180
 Db 115 CAGGCTCCAGGCGAGGGCTGGAGTGGTCTCAGCTATAGTAGTGGTGGTATCCACACA 174
 QY 181 TGTAGCCAGACTCCCTGAGGCGAGATTCACCATCTCCAGAGAGACGCCCAACACACA 240
 Db 175 TACTAGCCAGACTCAGTGAAGGCGGATTCACCATCTCCAGAGAGACGCCCAAGACTCA 234
 QY 241 CTGTTCTTCAATGAAGCTGAGCTGAGGACAGGCTGTCTATTACTGTGGGAG 299
 Db 235 CTGTTCTTCAATGAAGCTGAGCTGAGGACAGGCTGTCTATTACTGTGGGAG 293

RESULT 8
 US-09-864-761-31233
 ; Sequence 31233, Application US/09864761
 ; Patent No. US20020048763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharron G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; APPLICANT: Chen, Wensheng
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 ; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
 ; FILE REFERENCE: Aemica-X-1
 ; CURRENT APPLICATION NUMBER: US/09/864,761
 ; PRIOR FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: US 60/180,312
 ; PRIOR FILING DATE: 2000-02-04
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 09/632,366
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: GB 24263.6
 ; PRIOR FILING DATE: 2000-10-04
 ; PRIOR APPLICATION NUMBER: US 60/236,359
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00663
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00662
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00661
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00670
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: US 60/234,687
 ; PRIOR FILING DATE: 2000-09-21
 ; PRIOR APPLICATION NUMBER: US 09/608,408
 ; PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: US 09/774,203
 PRIOR FILING DATE: 2001-01-29
 NUMBER OF SEQ ID NOS: 49117
 SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
 SEQ ID NO 31233
 LENGTH: 311
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: MAP TO AB019439.1
 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.42
 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.51
 OTHER INFORMATION: EST HUMAN HIT: AW403220.1, EVALUATION 0.00e+00
 OTHER INFORMATION: NT HIT: L29155.1, EVALUATION 0.00e+00
 OTHER INFORMATION: SWISSPROT HIT: P01764, EVALUATION 3.00e-43
 US-09-864-761-31233
 Query Match 62.9%; Score 222.6; DB 9; Length 311;
 Best Local Similarity 86.6%; Pred. No. 1.9e-60;
 Matches 259; Conservative 0; Mismatches 34; Indels 6; Gaps 1;
 QY 1 GAGGTCCAGCTGTGGAGCTCTGGGGCGCTTGGCAAGCCCTGGGGGTCCTCAGACTC 60
 Db 12 GAGGTCCAGCTGTGGAGCTCTGGGGCGCTTGGCAAGCCCTGGGGGTCCTCAGACTC 71
 QY 61 TCTGCGCAGCTCTCCGGGTTCAAGTTCACTTCAATTAATCTATCATGACTGGGTCCGC 120
 Db 72 TCTGTCGAGCTCTG-----GATTCACCTTCAGTAGTATAGATGAATGGTCCGC 125
 QY 121 CAGGCTCCAGGCGAGGGCTGGAGTGGTCTCAGCTATAGTAGTGGTGGTATCCACACA 180
 Db 126 CAGGCTCCAGGCGAGGGCTGGAGTGGTCTCAGCTATAGTAGTGGTGGTATCCACACA 185
 QY 181 TGTAGCCAGACTCCCTGAGGCGAGATTCACCATCTCCAGAGAGACGCCCAACACACA 240
 Db 186 TACTAGCCAGACTCAGTGAAGGCGGATTCACCATCTCCAGAGAGACGCCCAAGACTCA 245
 QY 241 CTGTTCTTCAATGAAGCTGAGCTGAGGACAGGCTGTCTATTACTGTGGGAG 299
 Db 246 CTGTTCTTCAATGAAGCTGAGCTGAGGACAGGCTGTCTATTACTGTGGGAG 304
 RESULT 9
 US-10-038-591-29
 ; Sequence 29, Application US/10038591
 ; Publication No. US20040086503A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cohen, Bruce D.
 ; APPLICANT: Beebe, Jean
 ; APPLICANT: Miller, Penelope B.
 ; APPLICANT: Moyer, James D.
 ; APPLICANT: Corvalan, Jose R.
 ; APPLICANT: Gallo, Michael
 ; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
 ; FILE REFERENCE: ABX-PF2
 ; CURRENT APPLICATION NUMBER: US/10/038,591
 ; CURRENT FILING DATE: 2002-01-04
 ; PRIOR APPLICATION NUMBER: 60/259,927
 ; PRIOR FILING DATE: 2001-01-05
 ; NUMBER OF SEQ ID NOS: 60
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 29
 ; LENGTH: 296
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-038-591-29
 Query Match 62.6%; Score 221.6; DB 17; Length 296;
 Best Local Similarity 86.6%; Pred. No. 3.9e-60;
 Matches 258; Conservative 0; Mismatches 34; Indels 6; Gaps 1;
 QY 2 AGGTCCAGCTGTGGAGCTCTGGGGCGCTTGGCAAGCCCTGGGGGTCCTCAGACTCT 61

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Db      2 AGGTGAGCTGGTGGAGCTCTGGGGGAGGCTGGTCAAGCCCTGGAGGGTCCCTCGAGACTCT 61
Qy      62 CTTGCGCAGCTCCGGGTTCAGGTTCACTTCAATACTACTCATGACTGGTGGTCCGCC 121
Db      62 CTTGCGCAGCTCTG-----GATTCACTTTCAGTGACTACTCATGACTGGTGGTCCGCC 115
Qy      122 AGGCTCCAGGCGAGGGCTGGAGTGGGTCTCACGATTATAGTAGTGGTGGATCCCAT 181
Db      116 AGGCTCCAGGCGAGGGCTGGAGTGGGTCTCATCACTATAGTAGTGGTGGTACCATAT 175
Qy      182 GGTACGGAGCTCCGTGAAGGGAGATTCACTCTCCAGAGAAAGCCCAACACAC 241
Db      176 ACTACGCGAGACTCTGTGAAGGGCGATTCCACCTTCAGGGAACAGCCCAAGAACTCAC 235
Qy      242 TGTTCCTTCAATCAAGAGCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAG 299
Db      236 TGTATCTGCAATGAACAGCTGAGAGCGGAGGACGCGCGGTGTATTACTGTGCGAG 293

RESULT 10
US-10-251-215-20
; Sequence 20, Application US/10251215
; Publication No. US20030219839A1
; GENERAL INFORMATION:
; APPLICANT: Bowditch, Katherine S.
; APPLICANT: Kretz-Rommel, Anke
; TITLE OF INVENTION: ANTI-PDGF ANTIBODIES AND METHODS FOR PRODUCING ENGINEERED
; TITLE OF INVENTION: ANTI-PDGF ANTIBODIES
; FILE REFERENCE: 1087-36
; CURRENT APPLICATION NUMBER: US/10/251,215
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 60/323,537
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: US 60/323,544
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: US 60/379,980
; PRIOR FILING DATE: 2002-05-13
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 294
; TYPE: DNA
; ORGANISM: human
US-10-251-215-20

Query Match      62.0%; Score 219.4; DB 16; Length 294;
Best Local Similarity 86.0%; Pred. No. 1.9e-59;
Matches 257; Conservative 0; Mismatches 36; Indels 6; Gaps 1;

Qy      1 GAGGTGCGAGCTGGTGGAGCTCTGGGGGCGGCTTGGCAAGCCCTGGGGGTCCCTGAGACTC 60
Db      1 GAGGTGCGAACTGGTGGAGTCTGGGGGAGGCTGGTCAAGCCCTGGGGGTCCCTGAGACTC 60
Qy      61 TCCTGCGCAGCTCCGGGTTCAGGTTCACCTTCAATAAATACTACATGAGCTGGGTCCGC 120
Db      61 TCCTGTCCAGCTCTG-----GATTCACTTTCAGTAGCTATAGCATGAATGGGTCCGC 114
Qy      121 CAGGCTCAGGCGAGGCTGGAGTGGGCTCAAGTATTAGTAGTGGTGGTATCCCA 180
Db      115 CAGGCTCAGGGAAGGGCTGGAGTGGGCTCATCCATTAGTAGTGGTGGTATTA 174
Qy      181 TGGTACGAGACTCCGTGAAGGGCAGATTCCACATCTCCAGAGAAAGCCCAACACAC 240
Db      175 TACTACGAGACTCAGTGAAGGGCGGATTCCACATCTCCAGAGAAAGCCCAAGAACTCA 234
Qy      241 CTTTCCTTCAATGAACAGCTGAGAGCTGAGGACAGGGCTGTCTATTACTGTGCGAG 299
Db      235 CTGTATCTGCAATGAACAGCTGAGAGCCGAGCCGAGGACAGGGCTGTGTATTACTGTGCGAG 293

RESULT 11
US-10-324-493-15

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; Sequence 15, Application US/10324493
; Publication No. US20030124121A1
; GENERAL INFORMATION:
; APPLICANT: Plueneke, John
; TITLE OF INVENTION: USE OF INTERLEUKIN-4 ANTAGONISTS AND COMPOSITIONS THEREOF
; FILE REFERENCE: 3005-C
; CURRENT APPLICATION NUMBER: US/10/324,493
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US/09/847,816
; PRIOR FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/579,808
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/665,343
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/785,934
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 348
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: {1}..(348)
US-10-324-493-15

Query Match      61.9%; Score 219; DB 15; Length 348;
Best Local Similarity 78.8%; Pred. No. 2.7e-59;
Matches 277; Conservative 0; Mismatches 70; Indels 6; Gaps 1;

Qy      2 AGGTGCGAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAGCCCTGGGGGTCCCTGAGACTCT 61
Db      2 AGGTGCGAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCTGGGAGGTCCCTGAGACTCT 61
Qy      62 CTTGCGCAGCTCCGGGTTCAGGTTCACTTCAATACTACTCATGACTGGTCCGCC 121
Db      62 CTTGTTCCAGGCTCTG-----GATTCACTTTCAGTAGATATGCGATGCACTGGTCCGCC 115
Qy      122 AGGCTCCAGGCGAGGGCTGGAGTGGGTCTCAGCTGAGTTCACGATTATAGTAGTGGTGGATCCCA 181
Db      116 AGGCTCCAGGCGAGGGCTGGAGTGGGTGGCAATTATATGTTTGAAGGAATAATCAAT 175
Qy      182 GGTACCGAGACTCCGTGAAGGGCAGATTCAACATCTCCAGAGAAAGCCCAACACAC 241
Db      176 ACTATGCGAGACTCCGTGAAGGGCGGATTCAACCTCTCCAGAGCAATTCAGAAACACGC 235
Qy      242 TGTTCCTTCAATAAAGAACAGCTCAGAGCTCAGGACACGGCTGTCTATTACTGTGCGAGCT 301
Db      236 TGTATCTGGAATGAACAGCTCAGAGCCCTGAGAGCCGAGACACGGCTGTGTATTACTGTGCGAG 295
Qy      302 TGACTACAGGCTCTGACTCTCTGGGGCGAGGGAGTCTGGTCCAGCTCTCTCA 354
Db      296 GGAAGTACTACTTTGACTACTCTGGGGCGAGGAAACCTGGTCCAGCGTCTCTCA 348

RESULT 12
US-10-324-493-11
; Sequence 11, Application US/10324493
; Publication No. US20030124121A1
; GENERAL INFORMATION:
; APPLICANT: Plueneke, John
; TITLE OF INVENTION: USE OF INTERLEUKIN-4 ANTAGONISTS AND COMPOSITIONS THEREOF
; FILE REFERENCE: 3005-C
; CURRENT APPLICATION NUMBER: US/10/324,493
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US/09/847,816
; PRIOR FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/579,808
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/665,343
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/785,934

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Qy 1 GAGGTGCAGCTGTGGTGGAGTCTGGGGGGGGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTC 60
Db 1 GAGGTGCAGCTGTGGAGTCTGGGGGGGAAACTTGGTACAGCCTGGGGGGTCCCTGAGACTC 60
Qy 61 TCTGTGCGAGCTCCGGGTTCAGGTTCACTTCAATAACTACTACATGAGCTGGGTCCGC 120
Db 61 TCTGTGCGAGCTCTG-----GATTCACTTTAGCAGCTATGCCATGAGCTGGGTCCGC 114
Qy 121 CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTACGTTATTAGTAGTAGTGGTATCCCA 180
Db 115 CAGGCTCCAGGGAAAGGGGCTGGAGTGGGTCTCTTCTATTACTGGTAGTGGGGTAGCACA 174
Qy 181 TGGTACGAGACTCCGTGAAGGGCAGATTACCATCTCCAGAGAGAAAGCCCAACACACA 240
Db 175 TACTACGAGACTCCGTGAAGGGCGGTTACCATCTCCAGAGACAATTCCAAGACACG 234
Qy 241 CTGTTCTTCAATGAACAGCCTGAGAGCTGAGGACAGGGCTGTCTATTACTGTGGGAGC 300
Db 235 CTGTATCTGCAAAATGAACAGCCTGAGAGCCGAGGACACGGCCATTTTTTACTGTGCGAAA 294
Qy 301 TTGACTACAGG---GTCTGACTCTCTGGGGCAGGGAGTCTGTGTCAACCTCTCTCTCA 354
Db 295 GATACACGGGGGATCTTTCATATTGGGGCAGGGAAACCTGGTCACTCTCTCTCA 351

RESULT 14
US-10-460-595-1
; Sequence 1, Application US/10460595
; Publication No. US20040067532A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Li
; APPLICANT: Wei, Shuanghong
; APPLICANT: Hua, Shaohong B
; TITLE OF INVENTION: HIGH THROUGHPUT GENERATION AND AFFINITY MATURATION OF HU
; FILE REFERENCE: 25636-730
; CURRENT APPLICATION NUMBER: US/10/460,595
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: US 60/403,296
; PRIOR FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 296
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus human germline VH sequence (DP47)
US-10-460-595-1

Query Match 61.2%; Score 216.8; DB 13; Length 296;
Best Local similarity 85.6%; Pred.No.1.3e-58;
Matches 255; Conservative 0; Mismatches 37; Indels 6; Gaps 1e-1

Qy 1 GAGGTGCAGCTGTGGGAGTCTGGGGGGCGGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTC 60
Db 1 GAGGTGCAGCTGTGGAGTCTGGGGGGGCGCTTGGTACAGCCTGGGGGGTCCCTGAGACTC 60
Qy 61 TCTGTGCGAGCTCCGGGTTCAGGTTCACTTCAATAACTACTACATGAGCTGGGTCCGC 120
Db 61 TCTGTGCGAGCTCTG-----GATTCACTTTAGCAGCTATGCCATGAGCTGGGTCCGC 114
Qy 121 CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTACGTTATTAGTAGTAGTGGTATCCCA 180
Db 115 CAGGCTCCAGGGAAAGGGGCTGGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGTAGCACA 174
Qy 181 TGGTACGAGACTCCGTGAAGGGCAGATTACCATCTCCAGAGAGAAAGCCCAACACACA 240
Db 175 TACTACGAGACTCCGTGAAGGGCGGTTACCATCTCCAGAGACAATTCCAAGACACG 234
Qy 241 CTGTTCTTCAAAATGAACAGCCTGAGAGCTGAGGACAGGGCTGTCTATTACTGTGCGGA 298
Db 235 CTGTATCTGCAAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATTTACTGTGCGGA 292

RESULT 15
US-10-038-591-31
; Sequence 31, Application US/10038591
; Publication No. US20040086503A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/10/038,591
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 296
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-038-591-31

Query Match 61.2%; Score 216.8; DB 17; Length 296;
Best Local Similarity 85.6%; Pred. No. 1.3e-58;
Matches 255; Conservative 0; Mismatches 37; Indels 6; Gaps 1;
QY 1 GAGGTGACGTGGTGGAGTCTGGGGGGCTTTGGCAAGCCCTGGGGGGTCCCTGAGACTC 60
Db 1 GAGGTGACGTGGTGGAGTCTGGGGGGAGGCTTGGTACAGCCCTGGGGGGTCCCTGAGACTC 60
QY 61 TCCTGCGAGCCTCGGGGTTCAAGTTCACTTCAATAACTACTATGAGACTGGGTCCGC 120
Db 61 TCCTGTCAGCCTCTG-----GATTCACTTTAGCAGCTATGCCATGAGCTGGGTCCGC 114
QY 121 CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCACTGTTATTAGTAGTGGTATCCCA 180
Db 115 CAGGCTCCAGGGAGAGGGGCTGGAGTGGGTCTCAGCTATTAGTGGTGGTGGTAGCA 174
QY 181 TGGTACGACAGCTCCGCTGAAGGGCAGATTTCACCATCTCCAGAGAGAACGCAACACA 240
Db 175 TACTACGACAGCTCCGCTGAAGGGCCGGTTCAACCATCTCCAGAGACATTTCCAGAACACG 234
QY 241 CTGTTTCTTCAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGA 298
Db 235 CTGTATCTGCAATGAACAGCCTGAGAGCCGAGAGCCGAGGACACGGCCGTATATTACTGTGCGA 292

Search completed: June 19, 2004, 10:06:38
Job time : 287 secs